

**GENETIC DIVERGENCE STUDIES IN
FINGER MILLET (*Eleusine coracana* (L.)
Gaertn) GERMPLASM**

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B.Sc. (Ag.)

**MASTER OF SCIENCE IN AGRICULTURE
(GENETICS AND PLANT BREEDING)**



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FINGER MILLET (*Eleusine coracana* (L.)
Gaertn) GERMPLASM**

BY

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B.Sc. (Ag.)

THESIS SUBMITTED TO THE
ACHARYA N. G. RANGA AGRICULTURAL UNIVERSITY
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MAY, 2013

DECLARATION

I, **RAJIB DAS** hereby declare that the thesis entitled “**GENETIC DIVERGENCE STUDIES IN FINGER MILLET (*Eleusine coracana* (L.) Gaertn) GERMPLASM**” submitted to Acharya N.G. Ranga Agricultural University for the degree of **MASTER OF SCIENCE IN AGRICULTURE** is a result of the original research work done by me. I also declare that the thesis or part thereof has not been published earlier elsewhere in any manner.

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CERTIFICATE

Mr. RAJIB DAS has satisfactorily prosecuted the course of research and that the thesis entitled “**GENETIC DIVERGENCE STUDIES IN FINGER MILLET (*Eleusine coracana* (L.) Gaertn) GERMPLASM**” submitted is the result of original research work and is of sufficiently high standard to warrant its presentation to the examination. I also certify that the thesis or part thereof has not been previously submitted by him for a degree of any University.

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CERTIFICATE

This is to certify that the thesis entitled “**GENETIC DIVERGENCE STUDIES IN FINGER MILLET (*Eleusine coracana* (L.) Gaertn) GERMPLASM**” submitted in partial fulfilment of the requirements for the degree of **MASTER OF SCIENCE IN AGRICULTURE** of the Acharya N.G. Ranga Agricultural University, Hyderabad is a record of the bonafide research work carried out by **RAJIB DAS** under my guidance and supervision. The subject of the thesis has been approved by the Student’s Advisory Committee.

No part of the thesis has been submitted for any other degree or diploma or has been published. The published part has been fully acknowledged. All the assistance and help received during the course of investigation have been duly acknowledged by the author of the thesis.

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LIST OF SYMBOLS AND ABBREVIATIONS

%	:	per cent
<	:	less than
>	:	more than
ANOVA	:	Analysis of variance
C.D.	:	Critical difference
C.V.	:	Coefficient of variation
cm	:	centimeter
d.f.	:	degrees of freedom
<i>et al.</i>	:	and others
F ₁	:	First filial generation
g	:	gram
<i>Gca</i>	:	general combining ability
ha	:	hectare
<i>i.e.</i>	:	that is
kg	:	kilogram
m	:	meter
MSS	:	Mean Sum of Squares
No.	:	Number
r	:	Correlation coefficient
RBD	:	Randomized Block Design
t	:	tonne
<i>viz.</i>	:	namely
Vs.	:	versus

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ABSTRACT

A field experiment was conducted to estimate the genetic variability and genetic divergence in finger millet and to carry out yield component analysis through correlation and path analysis. Forty eight germplasm lines were sown in a randomized block design with three replications, during *kharif* 2012 at National Bureau of Plant Genetic Resources, Regional station, Rajendranagar, Hyderabad. The objective of the experiment was to identify divergent genotypes to use as donor parents in hybridization programmes.

On the basis of the mean performance of the genotypes among traits studied, the following were identified as promising lines for further crop improvement SNVD-11-118 which recorded highest mean grain yield per plant also possessed the maximum mean value for total productive tillers, CMLS-01-336-SEL-11 was recorded highest mean value for ear width and finger length, SRYA-333-SEL-2 recorded highest plant height, PR-202 for maximum no. of leaves, CMLS-01-336-SEL-08 for maximum main ear length, SRS-13436 for highest finger width, SRS-13433 for maximum no. of finger and NSS-7928-SEL-1 for grain yield per plot. The above mentioned genotypes will be useful for increased productivity.

The analysis of variance revealed significant differences among genotypes for all the characters. Studies of genetic variability revealed high phenotypic and genotypic coefficients of variation, heritability and genetic advance as percent of mean for the traits viz., main ear length, main ear width, grain yield per plant and grain yield per plot, indicating simple selection can be practiced for improvement of these characters.

The correlation analysis revealed that grain yield per plant showed positive significant association with no. of basal tillers, no. of productive tillers, main ear width, finger length, finger width, total fingers on the main ear and grain yield per plot.

Path coefficient analysis revealed that number of productive tillers per plant exerted the highest positive direct effect on grain yield per plant followed by main ear width, finger length, finger width and grain yield per plot along with significant positive correlation for all the above mentioned characters.

Therefore, it is emphasized to lay attention on traits like no. of basal tillers, no. of productive tillers, main ear width, finger length, finger width and grain yield per plot in crop improvement programme of finger millet in future.

The D^2 analysis was carried out for eleven characters which partitioned the forty eight genotypes into eight clusters. Maximum divergence was observed between cluster VI and VIII, while minimum was between cluster I and V. The maximum intra cluster distance was shown by cluster VIII.

Higher grain yield per plant was recorded for clusters are VII, I and II. Genotypes included in cluster VII is having highest mean value for grain yield per plant, total no. of basal tillers per plant and total productive tillers per plant. Cluster II is having highest mean value for no. of leaves on the main tiller and total fingers on the main ear. The genotypes SRYA-333-SEL-2 (VII) as this cluster had only one genotype which become automatic choice, BAR-174 and SNVD-11-118 (I), SRS-13447 and SRS-13433 (II) from these clusters having high mean values for grain yield per plant may be directly used for adaptation or may be used as parents in future hybridization programme.

Among the eleven quantitative characters studied the most important character contributing to the divergence was main ear length followed by total no. of fingers on the main ear, grain yield per plot, grain yield per plant, main ear width, total no. of basal tillers per plant, no. of leaves on the main tiller, total no. of productive tillers per plant, finger width, finger length. In order to select genetically diverse genotypes the material should be screened for the important traits viz., was main ear length, total no. of fingers on the main ear, grain yield per plot, grain yield per plant, main ear width, total no. of basal tillers per plant.

Chapter I

Introduction

Chapter I

INTRODUCTION

Finger millet (*Eleusine coracana* (L.) Gaertn) also known as birds foot millet, ragi or African millet is an annual plant widely grown as an important food crop in the arid areas of Africa and South Asia. It ranks third in importance among the millets after sorghum and pearl millet in India. It is a hardy crop that can be grown in diverse environments from almost at sea level in south India to high lands of Himalayas (altitudes of 1850 to 2300 meters) and from poor soils on hill slopes to rich soils in the Indogangetic plains. The crop provides food grain as well as straw, which is valued animal feed especially in rainfed areas.

In India it is very popularly known as ragi and is grown in an area of 2 million hectares with a production of 2.6 million tonnes. Finger millet provides staple food for a large section of farming community and economically weaker sections in many parts of India. Important finger millet growing states are Karnataka, Tamil Nadu, Andhra Pradesh, Maharastra, Orissa, Jharkhand, Chattishgarh and Uttarakhand

Finger millet species *coracana* belongs to family Graminae or Poacea. *Eleusine*, the generic name, is after *Eleusine* the Greek goddess of cereals. Common name 'Finger millet' is derived from the finger-like branching of the panicle. The cultivated *E. coracana* is a tetraploid ($2n=4x=36$) and has morphological similarity to both *E. indica* (L.) Gaertn ($2n=18$) and *E. africana* O. Byrne ($2n=36$). The cytological evidences indicate that *E. indica* has contributed one of the genomes (AA) to the cultivated *E. coracana* (AABB).

Finger millet is native to the Ethiopian highlands of central Africa and was introduced into Indian subcontinent approximately 3000 years ago. The long history of cultivation of finger millet in India under diverse agro-climatic conditions and the associated human and natural selection has resulted in generation of large variability giving India the status of secondary centre of diversity.

Ragi is commonly called as "Nutritious millet" as the grains are nutritionally superior to many cereals providing fair amount of proteins, minerals, calcium and vitamins in abundance to the people. It provides proteins, minerals, calcium and vitamins 8-10 times more than that of rice and wheat. It is the cheapest and preferred food crop of economically suppressed but physically hard working people. It is appreciated by the people, because it can digest slowly thereby furnish energy for hard work throughout the day. Finger millet

meets the first and most needs of mankind, the energy and hunger satisfaction. It leaves a sense of being well fed to any farmer. The protein of finger millet has been reported to possess a fairly high biological value, which is needed for the maintenance of nitrogen equilibrium of the body. The higher fibre content of finger millet helps in many ways as it prevents constipation, high cholesterol formation and intestinal cancer. Hence, people suffering from diabetics are advised to eat finger millet and other small millets instead of rice (Malleshi and Hadimani,1993).

Its nature of requirement of low inputs in terms of labour,technology, costs and high drought resistance and long storage life makes it a pro-poor and marginal farmer crop. Its small seeds can be stored safely for as long as 50 years without pest infestation, which makes it a traditional component of farmers risk mitigation strategies in drought prone regions. It is highly valued as a reserve food in the times of famine. Despite all these merits, this crop has been neglected from the main stream of crop improvement programme. One of the means to boost its production and productivity is to enhance utilization of finger millet.

Exploitation of genetic variability existing in the working germplasm is the first principle in the improvement of any crop. Analysis and utilization of available genetic diversity is a short-term strategy for developing improved cultivars for meeting immediate requirement of the farmers and the end users. The finger millet crop has a wide range of variation for its character.

Since yield is a complex trait, knowledge on the association of the different yield components with grain yield and interrelation among themselves is necessary. Selection of superior genotypes based on yield as such is difficult due to the integrated structure of plant in which most of the characters are interrelated and being governed by more number of genes. This necessitates a thorough knowledge on the nature of relationship prevalent between contributory characters and grain yield and the extent of genetic variability.

A study through correlation coefficients on the genotypic values provides dependable basis for selection. Correlation in conjunction with path analysis would give a better insight into cause and effect relationship between different pairs of characters. Therefore, the present investigation was undertaken with the following objectives,

1. To estimate variability parameters for yield and its components.

2. To estimate genetic diversity among lines using D^2 statistic.
3. To estimate the extent of association existing among different yield components and their relation with yield in these genotypes.
4. To identify the characters which are directly or indirectly influencing the grain yield based on path coefficient analysis.

Chapter II

Review of Literature

Chapter II

REVIEW OF LITERATURE

The phenotype of quantitative traits, in principle, is the joint product of genotype and environment. Hence, the estimates of variability and its heritable components for the yield contributing characters in the available germplasm are pre-requisites for a breeding programme for high yield.

The success of breeding programme depends on the quantum of genetic variability available for exploitation. The information on the type of variation in the available genetic material and the part played by the environment on the expression of plant characters is of prime importance for the appraisal of rate and magnitude of possible improvement. Several investigators have screened finger millet genotypes from different sources, which exhibited immense range of variation in morphological, physiological and biochemical traits that govern the performance. The literature related to the present study is reviewed in this chapter under the following headings

- 2.1 Genetic variability**
- 2.2 Correlation studies**
- 2.3 Path coefficient analysis**
- 2.4 Genetic divergence**

2.1 GENETIC VARIABILITY

Possibility of achieving improvement in any crop plants depends heavily on the magnitude of genetic variability. Phenotypic variability expressed by a genotype or a group of genotypes in any species can be partitioned into genotypic and environmental components. The genotypic component being the heritable part of the total variability, its magnitude for yield and its component characters influences the selection strategies to be adopted by the breeders.

Thakur and Saini (1995) conducted an experiment during summer season of 1989 and 1990 to study the variation in finger millet. High heritability and genetic advance (% of mean) were observed respectively for yield (59%, 124%), days to flowering (80%, 17.4%), plant height (56%, 13.2%) and days to maturity (79%, 28.9%).

Vadivoo *et al.* (1998) observed that thirty six genotypes of finger millet with varying seed colours revealed a wide range of protein and calcium contents. White seeded genotypes had higher protein contents, while brown seeded types had a wide range of values. The genotypic coefficients of variability were moderate and high for protein and calcium, respectively. High heritability coupled with high genetic advance indicated their governance by additive gene action.

Jain and Yadava (1999) concluded that genotypic and phenotypic coefficients of variation were high for incidence of leaf, neck and finger blast and moderate for grain yield, tillers/plant, harvest index and leaves/plant. All the blasts, together with ear length, vegetative period, number of stomata and harvest index, exhibited high heritability coupled with moderate to high genetic advance as a percentage of mean.

Bendale *et al.* (2002) observed that phenotypic variances were higher than genotypic variances. Phenotypic (PCV) and genotypic coefficients of variation (GCV) were high for number of tillers, number of effective tillers, grain yield per plant, straw yield per plant, and weight of grains of main earhead.

Tiwari *et al.* (2005) studied intra- and inter population variation of finger millet land races. They found a considerable level of intra and inter population variability was observed for most quantitative and qualitative traits like plant height, leaf number, length of flag leaf, finger branching, finger type and size, and spikelet shattering.

Sripichitt *et al.* (2006) found that the phenotypic and genotypic coefficients of variations varied in the orders of 8.05-31.23% and 6.52-24.21% in both cases for days to maturity and grain yield per plant, respectively. Heritability estimates ranged from 20% for grain-filling duration to 84% for days to heading. Values of expected genetic advance varied from 6.67-44.14% for grain-filling duration and finger width, respectively. Finger width and length exhibited high heritability coupled with high genetic advance.

John (2006) concluded that the varietal improvement for grain yield is mainly dependent upon the extent of genetic variability present in the population. High genotypic and phenotypic coefficient of variation was observed for number of productive tillers per plant, number of fingers per ear and total dry matter production. Moderate (53.19% for main ear length) to high (95.55% for harvest index) estimates of heritability (broad sense) was obtained for almost all the characters studied. Number of productive tillers per plant, number of fingers per ear, test weight, total dry matter production and harvest index

possessed high heritability coupled with high estimates of genetic advance, it can be suggested that additive gene effects for these characters are present, hence selection at phenotypic level for these traits would be more effective.

Prabhu *et al.* (2008) observed high heritability and high genetic advance for number of tillers and single plant yield, indicating the possibility of improvement for this trait by simple selection.

Sonnad *et al.* (2008) recorded that the trait grain yield per plant showed moderate genotypic and phenotypic coefficients of variability with high heritability and genetic advance as per cent of mean indicates it is controlled by additive gene action and less influenced by environment. Straw yield per plant had higher variability, heritability and genetic advance as per cent of mean. While other characters under study had low variability, high heritability and moderate to high genetic advance as per cent of mean

Kadam *et al.* (2009) found that PCV and GCV were high for plant height, days to 50 per cent flowering, flag leaf blade length, inflorescence length and yield. Heritability and genetic advance was high for leaf blade length, basal tillers and plant height.

Krishnappa *et al.* (2009) revealed involvement of both additive and dominance genetic variation with a preponderance of the latter in the expression of time to 50% flower, plant height and dry fodder weight per plant while only dominance genetic variation was operative in the expression of number of tillers per plant, number of fingers per ear and grain weight per plant. These results are discussed in relation to the adoption of suitable breeding and selection strategy for genetic enhancement of economic traits in finger millet.

Kumar and Gupta (2009) concluded that phenotypic variability was higher for all the traits except days to 50 and 90% flowering, seed hardness and protein content, which showed similar magnitude of genotypic variability. Maximum difference between phenotypic and genotypic variability was observed for number of seeds per main ear.

Shet *et al.* (2010) observed high PCV and GCV values for grain yield per plant, finger width and plant height and days to 50% flowering whereas low to moderate for all other characters. Plant height, finger length, test weight and grain yield per plant reported high broad sense heritability accompanied with high genetic advance.

Upadhyaya *et al.* (2011) found that finger millet core collection for grain nutrients and agronomic traits revealed a substantial genetic variability for grain Fe, Zn, calcium (Ca) and protein contents. Accessions rich in Zn content have significantly higher grain yield potential than those rich in Fe and protein content. Grain nutrient-specific accessions and

those contrasting for nutrient contents were identified for use in the strategic research and cultivar development in finger millet.

Priyadharshini *et al.* (2011) observed values of phenotypic coefficients of variability were greater than genotypic coefficients of variability for all the traits studied. High PCV and GCV were recorded for number of productive tillers per plant and moderate PCV and GCV for longest finger length, seed protein content and harvest index indicated large extent of genetic variability for these traits in the material. High heritability along with high genetic advance (% of mean) observed for plant height, number of productive tillers per plant, number of fingers per ear head, longest finger length, seed protein content, harvest index and single plant grain yield, indicating involvement of additive gene action for these.

Ganapathy *et al.* (2011) studied two hundred and forty finger millet germplasm accessions. The coefficient of variation at phenotypic (PCV) and genotypic (GCV) levels were high for productive tillers per plant and moderate for the traits viz., days to 50 percent flowering, plant height, finger numbers per ear, finger length and grain yield per plant. Low PCV and GCV were observed in the trait days to maturity. From the results, high heritability coupled with high genetic advance observed in days to 50 per cent flowering, plant height, productive tillers per plant, finger numbers per ear, finger length and seed yield per plant, which indicates the predominance of additive gene effects, in controlling these traits, early and simple selection could be exercised due to fixable additive gene effects

Dhamdhere *et al.* (2011) concluded that genotypic coefficient of variation was the major component of total variation. However, PCV was invariably higher than GCV for most of the characters studied. Crude fiber content showed high PCV followed by ear weight, iron content, straw weight and grain yield while plant height showed lowest PCV. Ear weight, straw weight and total biomass showed high heritability and high genetic advance while grain yield exhibited moderate heritability and high genetic advance. Plant height, number of tillers per plant, leaf number per plant and finger number showed low heritability.

2.2 CORRELATION STUDIES

The inter relationship of quantitative characters with yield determine the efficiency of selection in breeding programmes. It merely indicates the intensity of association. Phenotypic correlation reflects the observed relationship, while genotypic correlation underline the true relationship among characters. Selection procedures could be varied depending on the relative contribution of each.

The following paragraph gives review of literature on correlation in ragi.

Wolie and Dessalegn (2011) studied the associations among yield components using eighty-eight finger millet genotypes in an augmented randomized complete block experimental design with two replications. Accordingly, phenotypic and genotypic correlations among the traits and grain yield was significantly correlated with its component characters like plant height, number of ears per plant, number of fingers per ear, finger length, biomass yield, harvest index, and thousand kernel weight.

Muduli *et al.* (2012) performed correlation analysis in forty four micro-mutant lines of each of the two finger millet varieties VR 708 and GPU 26. Significant positive association of tillers/plant, fingers/ear and ear weight/plant with grain yield per plant and among themselves was observed in both sets of mutant lines

Nandini *et al.* (2010) indicated that grain yield has strong positive correlation with weight of main ear, 1000 seed weight and total tillers per plant in F₂ population.

Shinde *et al.* (2010) indicated positive and highly significant correlation with straw yield per plant, harvest index and weight of grains on main earhead at phenotypic and genotypic level, while number of fingers on main earhead at genotypic level only.

Bedis *et al.* (2006) reported that days to flowering, days to maturity, plant height, main ear length, number of fingers per ear and fodder yield were positively correlated with grain yield, suggesting that these are the major yield contributing traits in finger millet.

Anantharaju and Meenakshiganesan (2005) showed that grain yield has a positive and significant genotypic correlation with number of productive tillers and culm thickness.

Shanthakumar and Gouda (1997) found that grain yield was positively associated with ear weight per plant, productive tillers per plant, fingers per ear and grains per cm length of finger in F₂ and F₃ generation of the finger millet cross WR9A and U6.

Priyadharshini *et al.* (2011) found that Grain yield had positive correlation with number of productive tillers, finger length and harvest index.

Ganapathy *et al.* (2011) opined from the correlation analysis productive tillers per plant and finger length are the important yield contributing traits and due critical emphasis needs to be given to productive tillers per plant and finger length while selecting for grain yield improvement in finger millet.

Bandyopadhyay (2009) concluded that the correlation study indicated that sensitivity of cultivars to different temperature might be responsible to produce unexplained variability in the population through the appearance of new combinations, disappearance and re-appearance of some old combinations of characters.

John (2006) concluded that total dry matter production showed a positive and highly significant association with test weight (0.458). Grain yield showed a positive and highly significantly correlated with test weight (0.458), total dry matter production (0.585) and harvest index (0.597), hence grain yield could be improved through these characters. Significant positive regression coefficient was observed between grain yield and dry matter production ($r^2 = 0.3747$).

Kadam *et al.* (2009) opined from the correlation analysis that there were highly significant positive association with yield and almost all the growth and yield contributing characters except flag leaf blade width and exertion.

Bendale *et al.* (2002) observed that Grain yield had significant positive correlation with days to emergence of finger, days to maturity, finger length, weight of grains of main earhead, and straw yield per plant.

Sripichitt *et al.* (2006) observed that strongest positive association was observed between culm thickness and leaf blade width while the strongest negative association was found between 1000-grain weight and finger number. Grain yield per plant associated positively with productive tillers, 1000-grain weight, number of grains per spikelet and finger number and negatively associated with days to heading and maturity.

Shet *et al.* (2010) concluded from the correlation studies that grain yield per plant exhibited highly significant positive association with finger width and test weight.

Kumar and Gupta (2009) observed plant height, number of tillers per plant, number of panicles per main spike, length of main ear and number of seeds per main ear were significantly correlated with grain yield plant.

Dawa *et al.* (1996) evaluated forty genotypes of ragi for productivity related traits. From the correlation study they found grain yield/plant was positively associated with all the measured traits except flowering days.

Thakur and Saini (1995) conducted an experiment during summer season of 1989 and 1990 to study the association between different characters in finger millet. Days to germination, heading and maturity showed high negative association with grain yield, whereas fingers/plant showed high positive association.

Mahto *et al.* (2000) concluded that seed yield per plant had a significant positive correlation with days to 50 per cent flowering and a highly significant positive association with number of tillers per plant, days to maturity whereas plant height revealed a highly significant negative correlation with seed yield.

Satish (2003) observed that grain yield had positive and highly significant association with all the characters studied except plant height, days to 50 per cent flowering and days to maturity.

Marimuthu (1997) in a study comprising F₂ generation of four crosses observed that, grain yield had positive association with ear weight, number of productive tillers, fingers per ear, finger length, plant height and days to 50 per cent flowering.

Gowda (1997) reported positive association of grain yield with plant height, ear length, productive tillers and fingers per ear, but the magnitude was low.

Ravindran *et al.* (1996) indicated that productive tillers and fingers per ear had highly significant and positive association with grain yield.

Gowda (1996) reported positive and highly significant association of grain yield with plant height, number of productive tillers, fingers per ear and spikelet density.

Jain and Yadava (1999) showed significant positive association of blast resistance with plant height, leaf angle, leaf area and number of stomata per unit area. These traits also exhibited comparatively higher estimates of correlated response and relative selection efficiency. Thus, direct selection for blast resistance based on these traits would be most effective. Hence, selection of a dwarf plant with narrow and vertical leaves coupled with reduced number of stomata per unit area should increase blast resistance in finger millet.

Sonnad *et al.* (2008) recorded that grain yield per plant had strong positive association with finger number per ear and ear weight per plant at all the locations. Hence, simultaneous selection for these traits will be more reliable to develop high yielding genotypes. Ear head length and finger length had significant positive association with grain yield per plant.

2.3 PATH CO-EFFICIENT ANALYSIS

Assuming yield is a contribution of several characters which are correlated among themselves and to the yield, path coefficient analysis was developed (Wright, 1921; Dewey and Lu, 1959). Unlike the correlation coefficient which measures the extent of relationship, path coefficient measures, the magnitude of direct and indirect contribution of a component character to a complex character and it has been defined as a standardized regression coefficient which splits the correlation coefficient into direct and indirect effects.

Wolie and Dessalegn (2011) studied the direct and indirect influence of component characters on the grain yield of finger millet. Phenotypic path analysis showed biomass yield (0.835) and finger length (0.159), number of fingers per ear (0.016), and number of ears per plant (0.038) to exert positive direct effects on grain yield, while plant height, days to heading and days to maturity exhibited negative direct effects. Genotypic path analysis also revealed that biomass yield (2.240), number of tillers per plant (0.359) and finger length (0.242) exerted positive direct effects on grain yield.

Muduli *et al.* (2012) revealed that ear weight/plant had the highest direct effect on grain yield followed by days to flowering in VR 708, whereas, days to maturity followed by fingers/ear and ear weight/plant had the maximum direct contribution in GPU 26. As the direct effect of ear weight/plant in VR 708 was too high, its indirect effects via other traits were small or often negative and in GPU 26, it had low direct effect due to positive indirect effects via fingers/ear, tillers/plant and days to flowering.

Nandini *et al.* (2010) revealed that weight of main ear, 1000 seed weight showed positive direct effect on grain yield of main ear.

Shinde *et al.* (2010) reported that finger length, harvest index, number of fingers on main earhead and straw yield per plant had direct positive effect on grain yield at genotypic level. Selection programme based on number of fingers on main earhead and straw yield per plant will be effective for grain yield improvement in finger millet.

Bedis *et al.* (2006) indicated that the number of days to maturity, plant height, number of fingers per ear and fodder yield has direct positive contribution on grain yield. These traits deserve special emphasis in selection while selecting for improvement in grain yield of finger millet.

Anantharaju and Meenakshiganesan (2005) reported that number of productive tillers had a high positive direct effect and culm thickness and number of leaves had

moderate direct effects on grain yield. Finger length had high indirect effect on grain yield through the number of leaves and days to 50 % flowering.

Shanthakumar and Gouda (1997) found that ear weight per plant had the greatest direct effect on grain yield in F₂ and F₃ generation of finger millet cross WR9 and U6.

Marimuthu (1997) through the path coefficient analysis revealed that ear weight, number of productive tillers and finger length showed positive direct effects on grain yield.

Priyadharshini *et al.* (2011) reported that grain yield had positive correlation with number of productive tillers, finger length and harvest index. On the basis of path analysis, harvest index had high positive direct effect on grain yield and number of productive tillers and finger length had moderate direct effect and revealed true relationship of these traits with grain yield.

Ganapathy *et al.* (2011) concluded that productive tillers per plant and finger length are the important yield contributing traits, since these traits had significant positive correlation with grain yield and positive inter-correlation also themselves.

Kadam *et al.* (2009) opined from the path analysis that indirect effect of yield had masked the direct or indirect effect in almost all the characters except inflorescence width. The traits like yield, flag leaf blade length, flag leaf sheath length, inflorescence length, inflorescence width and 1000 grain weight be given due emphasis in selection programme of genotypes for substantial high yield improvement of finger millet.

Bendale *et al.* (2002) opined from association and path analysis, days to emergence of finger, days to 50% flowering, finger length, finger width, and weight of grains of main earhead had significant influence on grain yield per plant in finger millet.

Shet *et al.* (2010) concluded that productive tillers per plant had the highest positive direct effect followed by finger width and test weight on grain yield in these two crosses while finger number exerted low positive direct effect on grain yield.

Kumar and Gupta (2009) opined from path coefficient analysis that days to 50% flowering contributed maximum direct effect on grain yield per plant, followed by number of tillers per plant and 1000-grain weight. However, the indirect effects were also equally important.

Dawa *et al.* (1996) opined from the path analysis studies that the positive and direct effect of biological yield, harvest index and maturity duration on grain yield.

Thakur and Saini (1995) opined from the path coefficient analysis that per-se selection for yield would be highly effective, with simultaneous selection for lower days to germination, heading and maturity, and higher number of tillers and fingers per plant.

Mahto *et al.* (2000) noticed that number of tillers per plant and days to maturity had high positive direct effect on grain yield.

Satish (2003) observed high effect of ear weight per plant, straw yield per plant and flag leaf length and suggested to lay stress on these characters in selection programme for increasing yield.

Gowda (1997) observed high effect of productive tillers and fingers per ear on grain yield and suggested that due weightage has to be given to the characters in breeding programme for high yield. Harvest index contributed maximum positive direct effect to grain yield and duration of grain filling registered largest negative direct effect.

Ravindran *et al.* (1996) reported that number of productive tillers per plant and number of fingers on main ear had high direct effect on grain yield. While plant height showed negative and indirect effect on yield. They suggested that, selection programme based on number of productive tillers per plant and number of fingers on main ear will be effective for grain yield improvement.

2.4 GENETIC DIVERGENCE

The sum total of genes present in the genotypes is called germplasm. The study of genotype diversity and the information of core subsets are important activities in the conservation, evaluation and utilization of genetic resources (Brown, 1989).

Morphological similarity, ecogeographic diversity, phylogenetical relationship, Mahalanobis's D^2 statistics etc were the few earlier methods used for discriminating divergent populations, which are reinforced by more scientific and advanced biometric techniques viz., multivariate analysis based on principal component analysis, agglomerative cluster analysis.

Anantharaju and Meenakshiganesan (2008) conducted an experiment on fifty genotypes of finger millet for genetic divergence using cluster analysis for ten quantitative traits. The genotypes were grouped into fourteen clusters. Among the characters they studied, days to 50% flowering followed by number of leaves contributed more towards the total divergence.

Sheriff (1992) conducted study on nine metric traits in twenty *E. coracana* varieties grown under rainfed and irrigated conditions. Genetic divergence of twenty varieties of finger millet grown across two environments was assessed using Mahalanobis' D^2 statistic. They were grouped in to four clusters under rainfed and eleven under irrigated conditions. Genetic diversity is not related to geographic diversity. Days to flowering, days to maturity, plant height, ear length, ear weight and grain weight contributed maximum to genetic diversity in both environments.

Bedis *et al.* (2007) conducted an experiment on thirty seven finger millet strains to study the nature and magnitude of genetic divergence for seed yield and its components. D^2 values corresponding to the pairs of comparison between thirty seven cultivars ranging from 1.11 to 993.39 indicated a considerable amount of genetic diversity among the strains studied. The thirty seven strains were grouped into seven clusters, the cluster means revealed that days to flowering, days to maturity, plant height, number of productive tillers per plant, main ear length, number of fingers per ear, and fodder and grain yield per plant are important characters towards maximum divergence.

Sripichitt *et al.* (2006) conducted study on sixty-four accessions (960 individuals) of landraces collected from five former regions of Ethiopia and Eritrea covering different agro-ecologies were characterized for growth habit, ear shape, grain shape, grain surface, grain color and pericarp persistence. Overall characters revealed intermediate to high diversity ranging from 0.60 for pericarp persistence to 0.99 for grain surface. Ear shape grain shape and grain surface showed different levels of diversity among regions as opposed to growth habit, grain color and pericarp persistence whose variations were attributed to among accessions. The overall mean diversity estimate was high ($H'=0.82$). Generally, the result revealed the existence of a vast range of diversity in the indigenous finger millet germplasm.

Vadivoo *et al.* (1998) grouped thirty six genotypes into eight clusters. Clustering pattern failed to indicate any relationship between genetic diversity and geographic diversity. Based on genetic diversity and performance, the genotypes MS 1168, MS 174 and CO 13 were found to be suitable for use as parents in a hybridization program for improving yield; the genotypes MS 1168, MS 174 and MS 2869 for protein and Malawi 1915 and CO 11 for calcium. Protein and calcium contents contributed less to genetic divergence.

Kumar *et al.* (2010) grouped one hundred and forty diverse genotypes of finger millet into ten non-overlapping clusters. The inter-cluster distance varied from 16.85 between clusters X and I to 1.94 between clusters III and VIII. Genetic diversity was observed to be independent of the geographical origin of the genotypes.

Satish *et al.* (2007) conducted a study on finger millet to assess extent of genetic diversity involving 178 genotypes of finger millet for productivity traits. Study revealed that the genetic diversity did not relate to geographic origin. All the genotypes were grouped into ten different clusters. The inter cluster distance revealed that cluster 2 and 5 were found to be highly divergent. Florets number per spikelet contributed maximum to the divergence. Among all the clusters, cluster 7 showed highest cluster mean across the fifteen traits followed by cluster 5, 8 and 4 indicating presence of most promising genotypes in them. Selection of parents for hybridization to get desirable recombinants has been suggested.

Kadam (2008) grouped seventy genotypes in 8 clusters. The higher inter cluster distance was observed between cluster VIII and V followed by that between cluster VI and II, suggesting more variability in genetic makeup of genotypes included in these clusters. Cluster III had the highest mean values for grain yield/plant, 1000-grain weight, panicle branch number, and flag leaf blade width. Cluster VIII was the second highest for grain yield plant (g) and for exertion peduncle length and basal tiller, plant height, and days to 50% flowering followed by flag leaf blade length contributed maximum towards the total divergence. There were 4 solitary clusters and in the remaining clusters the genotypes varied from 2 to 4 numbers. Parallelism was observed between geographical diversity and genetic diversity

Suryakumar (1998) studied forty nine finger millet genotypes grouped into 10 clusters. Cluster analysis revealed that geographical diversity was not related to genetic diversity. The genotypes from the clusters II, X, V and VII having moderate to high genetic divergence coupled with high mean performance may be selected for yield and its important components such as productive tillers and straw yield for better recombination.

Lule *et al.* (2012) concluded that the trend of quantitative trait diversity revealed that the highest genetic diversity were observed at the lowest level (among landrace populations) followed among the regions or countries of origin and least among altitude

classes. This leads to suggest, taking more samples within a locality or population would be a better approach to capture the range of variation in finger millet population.

Prabhu *et al.*(2008) grouped one hundred fifty finger millet germplasm into 18 cluster based on based on genetic distance. Fourteen solitary clusters were superior viz., II, III, V, VI, VIII, X, XI, XII, XIII, XIV, XV, XVI, XVII and XVIII. Intercrossing between genotypes of these diverse clusters would generate a broad spectrum of variability for effective selection in the segregating generations for the development of high yielding cultivars.

Sahu and Pradhan (2012) grouped thirty finger millet genotypes into 12 clusters out of which, cluster 1 had six genotypes, cluster II seven genotypes, clusters III and V three genotypes each, clusters IV, VI and VII two genotypes each and clusters VIII to XIII consisted of one genotype each. The inter cluster distance was highest between cluster IV and VII followed by cluster IV and XII. The highest means for grain yield were observed in cluster X (OEB 71) and cluster VI and for number of productive tillers/plant were observed in cluster VIII. Custer XII (VL 149) had the highest mean for plant height, fingers/ear and ear length. The genotypes of these superior clusters can be effectively used in breeding programs. Among the characters, days to maturity followed by days to flowering and plant height contributed more towards the total divergence.

Chapter III

Materials and Methods

Chapter III

MATERIALS AND METHODS

The present investigation was undertaken at the National Bureau of Plant Genetic Resources, Rajendranagar, Hyderabad with the four objectives, viz., (1) To estimate variability parameters for yield and its components. (2) To estimate the extent of association existing among different yield components and their relation with yield in these germplasm lines (3) To identify the characters which are directly or indirectly influencing the grain yield based on path coefficient analysis (4) To estimate genetic diversity among lines using D^2 statistic.

3.1 MATERIALS

The experimental material comprised of 48 germplasm lines of finger millet (Table 3.1). These lines were collected from National Bureau of Plant Genetic Resources, Regional station, Rajendranagar, Hyderabad-30.

3.1.1 Plant material for genetic diversity assessment

The experimental plant material for genetic diversity assessment are given in Table 3.1.

3.2 METHODS

3.2.1 Morphological characterization

In the present investigation, the morphological data were recorded for genetic diversity studies from five plants selected randomly in each replication. Observations on the following characters were recorded at the different stages of crop growth period for genetic diversity assessment.

1. Plant height (cm)

The height of the main tiller from the ground level to the top of the ear head was recorded in centimeters at maturity and mean was computed.

2. No. of basal tillers per plant

Tiller number was counted from each tagged plants and the mean of five plants was computed as tillers per plant.

Table 3.1 Experimental material of 48 genotypes of finger millet

SL. No.	Genotypes	Source	SL. No	Genotypes	Source
1	SNVD-11-5	NBPGR Regional Research Station	25	CMLS-01-336-SEL-06	NBPGR Regional Research Station
2	SNVD-11-15	NBPGR Regional Research Station	26	CMLS-01-336-SEL-07	NBPGR Regional Research Station
3	snvd-11-28	NBPGR Regional Research Station	27	CMLS-01-336-SEL-08	NBPGR Regional Research Station
4	SNVD-11-38	NBPGR Regional Research Station	28	CMLS-01-336-SEL-09	NBPGR Regional Research Station
5	SNVD-11-41	NBPGR Regional Research Station	29	GPU-45	NBPGR Regional Research Station
6	SNVD-11-54	NBPGR Regional Research Station	30	CMLS-01336-SEL-11	NBPGR Regional Research Station
7	SNVD-11-72	NBPGR Regional Research Station	31	CMLS-01-336-SEL-12	NBPGR Regional Research Station
8	SNVD-11-77	NBPGR Regional Research Station	32	NSS-7928-SEL-1	NBPGR Regional Research Station
9	GPU-67	NBPGR Regional Research Station	33	NSS-7928-SEL-2	NBPGR Regional Research Station
10	SNVD-11-88	NBPGR Regional Research Station	34	NSS-7928-SEL-3	NBPGR Regional Research Station
11	SNVD-11-89	NBPGR Regional Research Station	35	NSS-7928-SEL-4	NBPGR Regional Research Station
12	SNVD-11-99	NBPGR Regional Research Station	36	PSR-10095-SEL-1	NBPGR Regional Research Station
13	SNVD-11-112	NBPGR Regional Research Station	37	PSR-10121	NBPGR Regional Research Station
14	PR-202	NBPGR Regional Research Station	38	SRYA-333-SEL-1	NBPGR Regional Research Station
15	AR-1	NBPGR Regional Research Station	39	SRYA-333-SEL-2	NBPGR Regional Research Station
16	SNVD-11-118	NBPGR Regional Research Station	40	SRYA-333-SEL-3	NBPGR Regional Research Station
17	AR-2	NBPGR Regional Research Station	41	SRS-13426	NBPGR Regional Research Station
18	AR-3	NBPGR Regional Research Station	42	SRS-13433	NBPGR Regional Research Station
19	SRS-13466	NBPGR Regional Research Station	43	SRS-13434	NBPGR Regional Research Station
20	AR-4	NBPGR Regional Research Station	44	SRS-13435	NBPGR Regional Research Station
21	AR-5	NBPGR Regional Research Station	45	SRS-13436	NBPGR Regional Research Station
22	BAR-174	NBPGR Regional Research Station	46	SRS-13448	NBPGR Regional Research Station
23	CMLS-01-336-SEL-01	NBPGR Regional Research Station	47	SRS-13439	NBPGR Regional Research Station
24	CMLS-01-336-SEL-03	NBPGR Regional Research Station	48	SRS-13447	NBPGR Regional Research Station

3. No. of leaves in main tiller

Total no. of leaves in main tiller was counted and mean was taken at maturity.

4. Productive tillers per plant

Number of basal tillers bearing the matured ears was counted from each of five tagged plants and average per plant was taken.

5. Main ear length (cm)

Length of main ear was measured in centimeter and mean was computed from five Plants.

6. Main ear width(cm)

Width of main ear was measured in centimeter and mean was computed from five plants

7. Finger length (cm)

Length of the longest finger on main tiller was measured in centimeter and mean of five plants was computed.

8. Finger Width (cm)

Width of each finger on main ear was taken and mean of five plants was computed.

9. Fingers number per ear

The number of fingers on main ear of each tagged plant was counted and averaged per plant.

10. Grain yield per plant (g)

Grains harvested from the five selected plants of each replication were dried and weighed. The average grain weight of five plants was expressed as grain yield per plant in grams.

11. Grain yield per plot(g)

Grain harvested from each replication was threshed separately and weighed.

12. Nodal Pigmentation

Nodal pigmentation was counted on the basis of their presence or absence in the germplasm lines.

13. Degree of lodging at maturity

Degree of lodging was counted according to susceptibility or resistance of plant to lodging during maturity.

14. Senescence/stay green colour at maturity

Green colour at maturity was counted on the basis of scoring against presence or absence.

15. Grain colour

Grain colour of five plants in each replication was counted by naked eye.

3.2.2 STATISTICAL ANALYSIS

The data collected for the above mentioned characters were subjected to the following statistical analysis with the help of appropriate standard statistical procedures as mentioned in the following sub-headings.

1. Analysis of variance
2. Estimation of genetic parameters like genotypic and phenotypic coefficients of variation, heritability and genetic advance
3. Estimation of correlation coefficients
4. Direct and indirect effects of characters using path coefficient analysis
5. Estimation of genetic divergence using Mahalanobis's generalized distances (D^2)

3.2.2.1 Analysis of Variance

Before proceeding to the biometrical genetic analysis of the data, the genotypic differences among the entries were tested. Further analysis was carried out only when the mean squares due to genotypes were significant. Hence the data for different characters were statistically analyzed for significance by using analysis of variance technique described by Panse and Sukhatme (1985). The adopted design was Randomized Block Design (RBD) replicated thrice.

The linear mathematical model:

$$Y_{ij} = \mu + g_i + r_j + e_{ij}$$

Where,

Y_{ij} = phenotypic observation of i^{th} genotype in j^{th} replication

μ = general mean

g_i = effect of i^{th} genotype

r_j = effect of j^{th} replication

e_{ij} = random error associated with i^{th} genotype and j^{th} replication.

Table: 3.2 The structure of analysis of variance (ANOVA) carried for each character was indicated below:

Source	S.S.	Degrees of freedom	Mean sum of squares	F-ratio
Replication	P	(r-1)	$M'r$	$M'r/M'e$
Treatment	Q	(t-1)	$M't$	$M't/M'e$
Error (e)	R	(r-1)(t-1)	$M'e$	
Total	S	(tr-1)	TMSS	

d.f. : degrees of freedom; SS : sum of squares; MSS : mean sum of squares

where,

r = number of replications

t = number of treatments

P = Replications sum of squares

Q = Treatments sum of squares

R = Error sum of squares

S = Total sum of squares

$M r'$, $M t'$, $M e'$ stands for mean sum of squares due to replications, treatments and error respectively. The significance of mean sum of squares for each character was tested against the corresponding error degrees of freedom using 'F' Test (Fisher and Yates, 1967).

i. Estimation of mean values, standard error, critical difference and coefficient of variation (analysis of means)

Mean values were calculated as averages over replications for each respective treatments. The comparison between any two treatments mean were performed by computing least significant difference (L.S.D.) or critical difference (C.D.) at 0.05 to 0.01 level of probability. The difference between any two treatment means was recorded as significant if they were greater than C.D.

$$\begin{aligned} \text{C.D.} &= \text{S.E.} \times t_{edf} \\ &= (\sqrt{2 M e' / r}) \times t_{edf} \end{aligned}$$

Where,

S.E. = standard error of the difference of the treatment means to be compared
 $= \sqrt{2 M e' / r}$
 t_{edf} = student's tabulated value at 5% and 1% level of significance at error degrees of freedom for the error mean square.

i. Coefficient of Variation (C. V.)

The Coefficient of variation is a unit less measurement and is used for comparing the extent of variation between different characters with different scales. It is the ratio of the standard deviation to the grand mean or experimental mean of the character.

$$\text{C.V.} = \frac{\sqrt{M e'}}{\bar{X}}$$

where,

$\bar{X}$ = Grand mean

3.2.2.2 Estimation of components of variances and genetic parameters

3.2.2.2.1 Estimation of components of variances

From the analysis of variance table, the mean sum of squares between genotypes will consist of the variances (i) due to genotypic differences and (ii) due to the environmental variation among the individuals of each genotype. Therefore, the genotypic

and phenotypic variances were calculated as per the formula given by Burton and Devane (1953).

$$\text{Environmental variance, } \sigma_e^2 = M e'$$

$$\text{Genotypic variance, } \sigma_g^2 = \frac{M t' - M e'}{r}$$

$$\text{Phenotypic variance, } \sigma_p^2 = \sigma_g^2 + \sigma_e^2$$

3.2.2.2.2 Estimation of genetic parameters

i. Phenotypic and genotypic co-efficients of variation

The components of variances were used to estimate genetic parameters like phenotypic and genotypic co-efficients of variation (PCV and GCV) as per the formulae given by Burton and De Vane (1953)

$$\text{GCV} = \frac{\sqrt{GV}}{\bar{X}} \times 100$$

$$\text{PCV} = \frac{\sqrt{PV}}{\bar{X}} \times 100$$

Where,

GCV = Genotypic coefficient of variation

PCV = Phenotypic coefficient of variation

GV = Genotypic variance

PV = Phenotypic variance

$\bar{X}$ = General mean of character

Categorization of the range of variation was followed as reported by Sivasubramanian and Menon (1973).

Low : Less than 10%

Moderate : 10 to 20%

High : More than 20%

ii. Heritability in broad sense [$h^2(b)$]

Heritability in the broad sense refers to the proportion of genotypic variance to the total observed variance in the total population. Heritability [$h^2(b)$] in the broad sense was calculated according to the formula given by Allard (1960) and expressed in percentage.

$$h^2(b) = \frac{\text{Genotypic variance, } (\sigma^2_g)}{\text{Phenotypic variance, } (\sigma^2_p)} \times 100$$

As suggested by Johnson *et al.* (1955) the range of heritability estimates were categorized as:

Low	:	0-30%
Medium	:	above 30-60%
High	:	above 60%

iii. Genetic advance (GA)

Genetic advance refers to the expected genetic gain or improvement in the next generation by selecting superior individuals under certain amount of selection pressure. From the heritability estimates the genetic advance was estimated by the following formula given by Burton (1952).

$$GA = K \cdot h^2(b) \cdot \sigma_p$$

Where,

GA = Expected genetic advance

K = Selection differential, the value of which is 2.06 at 5% selection intensity

σ_p = Phenotypic standard deviation

$h^2(b)$ = Heritability in broad sense

iv. Genetic advance as percent of mean (GAM)

In order to visualize the relative utility of genetic advance among the characters, genetic advance as percent for mean (GAM) was computed.

$$GAM = \frac{GA}{\text{Grand mean, } (\bar{X})} \times 100$$

The range of genetic advance as percent of mean was classified as suggested by Johnson *et al.* (1955).

Low	:	less than 10 %
Moderate	:	10-20 %
High	:	more than 20 %

3.2.2.3 Estimation of correlation co-efficients

Character association refers to the association of characters *i.e.*, a change in one character is accompanied by a change in the other character. The data on eleven quantitative characters were utilized for the computation of phenotypic and genotypic correlation co-efficients between grain yield and yield contributing traits of forty eight grmplasm lines in finger millet.

Phenotypic and genotypic correlation co-efficients were calculated for the characters by working out the variance components of each character and the covariance components for each pair of characters using the formulae suggested by Al-Jibouri *et al.* (1958).

$$\text{Genotypic correlation co-efficient, } (r_g) = \frac{\text{Cov } x \text{ } y \text{ (genotypic)}}{\sqrt{(\text{Var } x) \cdot (\text{Var } y) \text{ (genotypic)}}}$$

Where,

$$\text{Genotypic variance} = \frac{\text{Treatment MS} - \text{Error MS}}{\text{Number of replication}}$$

Similarly,

$$\text{Genotypic covariance} = \frac{\text{Treatment Cov} - \text{Error Cov}}{\text{Number of replications}}$$

$$\text{Phenotypic correlation coefficient (r}_p\text{)} = \frac{\text{Cov } xy \text{ (phenotypic)}}{\sqrt{(\text{Var } x) (\text{Var } y) \text{ (phenotypic)}}}$$

The values of genotypic correlation exceeding unity should be considered as unit only (of same sign). To test the significance of correlation coefficients, the estimated values were compared with the table values of correlation coefficients (Fisher and Yates, 1967) at 5 per cent and 1 per cent levels of significance with (n-2) degrees of freedom, where 'n' is the number of pairs of observations used in the experiment.

3.2.2.4 Path co-efficient analysis

The use of path coefficient analysis explains cause and effect relationship among the variables. It is a standardized partial regression coefficient and as such measures the direct influence of one variable upon another and permits the separation of the correlation coefficients into components of direct and indirect effects (Dewey and Lu, 1959). This method permits breeder to identify relatively important components of a variable, on the basis of their direct and indirect influences.

The direct and indirect effects both at genotypic and phenotypic level were estimated by taking grain yield per plant as dependent variable using path coefficient analysis suggested by Wright (1921) and Dewey and Lu (1959).

The following set of simultaneous equations were formed and solved for estimating various direct and indirect effects.

$$r_{1y} = P_{1y} r_{11} + P_{2y} r_{12} + P_{3y} r_{13} \dots \dots \dots + P_{ny} r_{1n}$$

$$r_{2y} = P_{1y} r_{21} + P_{2y} r_{22} + P_{3y} r_{23} \dots \dots \dots + P_{ny} r_{2n}$$

$$r_{ny} = P_{1y} r_{n1} + P_{2y} r_{n2} + P_{3y} r_{n3} \dots \dots \dots + P_{ny} r_{nn}$$

Where,

1, 2 n = Independent variable

y = Dependent variable (yield per plant)

$r_{1y} \ r_{2y} \ . \ . \ . \ . \ . \ . \ r_{ny}$ = Coefficient of correlation between causal factors '1' to 'n' on dependent character Y

$P_{1y} \ P_{2y} \ . \ . \ . \ . \ . \ P_{ny}$ = Direct effect of characters '1' to 'n' on character Y

The above equations can be written in matrix form as:

$$\begin{array}{ccc}
 \text{A} & \text{C} & \text{B} \\
 \left(\begin{array}{c} r_{1y} \\ r_{2y} \\ : \\ : \\ r_{ny} \end{array} \right) & \left(\begin{array}{ccccc} 1 & r_{12} & r_{13} & \dots\dots\dots r_{1n} \\ r_{21} & 1 & r_{23} & \dots\dots\dots r_{2n} \\ : & : & : & \\ : & : & : & \\ r_{n1} & r_{n2} & r_{n3} & \dots\dots\dots 1 \end{array} \right) & \left(\begin{array}{c} P_{1y} \\ P_{2y} \\ : \\ : \\ P_{ny} \end{array} \right)
 \end{array}$$

A and B vector values are known. Hence, to calculate C vector

$$B = [C]^{-1} A$$

where ,

$$C^{-1} = \left(\begin{array}{ccccc} c_{11} & c_{12} & c_{13} & \dots\dots\dots c_{1n} \\ c_{21} & c_{22} & c_{23} & \dots\dots\dots c_{2n} \\ : & : & : & : \\ : & : & : & : \\ c_{n1} & c_{n2} & c_{n3} & \dots\dots\dots c_{nn} \end{array} \right)$$

Direct effects were as follows:

$$P_{1y} = \sum_{i=1}^k c_{1i} r_{iy}$$

$$P_{2y} = \sum_{i=1}^k c_{2i} r_{iy}$$

$$P_{ny} = \sum_{i=1}^k c_{ni} r_{iy}$$

Residual effect (PR_y), which measures the contribution of characters not considered, in the causal scheme was obtained as:

$$\text{Residual effect } (PR_y) = \sqrt{1 - r^2}$$

Where,

$$r^2 = (P_{1y} r_{1y} + P_{2y} r_{2y} + \dots + P_{ny} r_{ny})$$

$$P_{ny} = \text{Direct effect of } x_n \text{ on } Y$$

$$r_{ny} = \text{Correlation coefficient of } x_n \text{ on } y.$$

3.2.2.5 Estimation of genetic divergence using Mahalanobis's generalized distances (D^2)

The genetic divergence between forty eight genotypes was estimated using Mahalanobis's (1936) D^2 statistic technique.

D^2 value between i^{th} and j^{th} genotypes for 'p' characters was calculated as:

$$D^2_{ij} = \sum_{t=1}^p (\bar{Y}_{it} - \bar{Y}_{jt})^2$$

Where,

$$Y_{it} = \text{Uncorrelated mean values of } i^{\text{th}} \text{ genotype for 't' character}$$

$$Y_{jt} = \text{Uncorrelated mean values of } j^{\text{th}} \text{ genotype for 't' characters and}$$

$$D^2_{ij} = D^2 \text{ between } i^{\text{th}} \text{ and } j^{\text{th}} \text{ genotype}$$

The various steps involved in estimation of D^2 values are given below:

3.2.2.5.1 Test of significance

After testing the differences between genotypes for each of the characters, a simultaneous test for significance for differences in the mean values of a number of correlated variations with regard to the pooled effect of characters was carried out by using 'V' statistic which in turn utilizes Wilk's 'Λ' criterion. The sum of squares and sum of product of *error* + *genotype* were used for this purpose. The estimation of 'Λ' (Wilk's criterion) was done using the following relationship.

$$\Lambda = \frac{|W|}{|S|}$$

Where,

Λ = Wilk's criterion

|W| = Determinant of error matrix and

|S| = Determinant of error + variety matrix

The significance of Λ was tested by V (stat.). The value of 'V' statistic was worked out using Wilk's lambda criterion.

$$V(\text{stat.}) = -m \log_e \Lambda = -\left(n - \frac{p+q+1}{2}\right) \log_e \Lambda$$

Where,

m = n - (p+q+1)/2

p = number of variables (or) characters

q = number of genotypes -1 (or degrees of freedom for population)

n = degrees of freedom for error + genotypes

e = 2.7183

or $\log_e \Lambda = 2.3026 \log_{10} \Lambda$

V (stat.) is distributed as χ^2 with 'pq' degrees of freedom. The tabulated value of χ^2 for 'pq' degrees of freedom at 5 per cent level is used to compare with the above calculated value of χ^2 for testing the significance.

When *d.f.* were beyond 100, then the tabulated χ^2 value is calculated by the formula as given by Singh and Chaudhary (1977).

$$Z = \sqrt{2 \chi^2} - \sqrt{2n-1}$$

Where, Z = Tabulated χ^2 value

n = number of degrees freedom

3.2.2.5.2 Transformation of correlated variables

In the present model, computation of D^2 values were reduced to simple summation values of the differences in mean values of various characters of the two genotypes i.e., $\sum d_i^2$. Therefore, transformation of correlated variables to uncorrelated ones was done before working out the D^2 values. Transformation was done by using pivotal condensation method.

3.2.2.5.3 Computation of D^2 values

For a given combination of 'i' and 'j' genotype, the mean deviation viz., $Y_{it} - Y_{jt}$ for $t = 1, 2, \dots, 'p'$ variables were computed and the D^2 values were calculated as sum of squares of deviations i.e.,

$$D^2_{ij} = \sum_{t=1}^p (\bar{Y}_{it} - \bar{Y}_{jt})^2$$

Where,

$$\begin{aligned} Y_{it} &= \text{Uncorrelated mean values of } i^{\text{th}} \text{ genotype for 't' character} \\ Y_{jt} &= \text{Uncorrelated mean values of } j^{\text{th}} \text{ genotype for 't' character} \\ D^2_{ij} &= D^2 \text{ between } i^{\text{th}} \text{ and } j^{\text{th}} \text{ genotype} \end{aligned}$$

3.2.2.5.4 Testing the significance of D^2 values

The D^2 values obtained for a pair of genotypes was taken as the calculated value of χ^2 and was tested against the tabulated value of χ^2 for 'p' degrees of freedom, where 'p' was the number of characters considered.

3.2.2.5.5 Contribution of individual characters towards divergence

In all the combinations each character was ranked on the basis of their contribution towards divergence between two entries ($d_i = Y_{it} - Y_{jt}$). Rank 1 was given to the highest

mean difference and rank 'p' to the lowest difference, where 'p' is the total number of characters considered.

Percentage contribution of each character (X) towards genetic divergence was calculated using the formula:

$$\text{Percentage contribution of character, } X = \frac{N}{M} \times 100$$

Where,

N = Number of genotype contributions where the character was ranked first

M = All possible combinations of genotypes considered

3.2.2.5.6 Grouping of genotypes into various clusters

Grouping of genotypes into different clusters was done using Tocher's method as described by Rao (1952). The criterion used in clustering by this method is that any two genotypes belonging to the same cluster should show at least on an average smaller D^2 value among themselves than those belonging to different clusters.

The first step in grouping the genotypes into different clusters was to arrange the genotypes in the order of their relative distance from each other. For this purpose, D^2 values of all combinations of each genotype were arranged in increasing order of their magnitude in a tabular form as described by Singh and Chaudhary (1977). To start with the two genotypes having the smallest distance from each other were considered first to which a third population having the smallest average D^2 value from the first two genotypes was added. Similarly, next nearest fourth genotype was considered and this procedure was continued. At certain stage where it was felt that after adding a particular genotype, there was abrupt increase in the average D^2 value, that population was not considered for including in that cluster. The group of the first cluster was then omitted and the rest was treated in a similar way. This process was continued till all the genotypes were included into one or other clusters.

3.2.2.5.7 Average intra cluster distance

For the measurement of intra cluster distance, the formula used was $\Sigma D_i^2 / n$.

Where,

ΣD_i^2 = Sum of distances between all possible combinations (n) of the populations
included in a cluster

n = Number of genotypes included in a cluster

3.2.2.5.8 Average inter-cluster distance

Clusters were taken one by one and their distance from other clusters was calculated. The distance between two clusters was the sum of D^2 values between the members of one cluster to each of the member of other cluster divided by the product of number of genotypes in both the clusters under consideration.

The square root of the average D^2 value gave the genetic distance 'D' between the clusters. Based on D values (inter cluster distance) the scale given by Rao (1952) for rating of the distance was adopted and the cluster diagram was prepared.

$$\text{Average inter cluster distance} = \frac{D^2}{n_1 \times n_2}$$

Where,

n_1 and n_2 are the number of genotypes in cluster 1 and cluster 2, respectively.

Category	'D' values
Closely related	Below 22
Moderately divergent	Between 22 and 30
Highly divergent	Above 30

Chapter IV

Results and Discussion



Fig: 1. Field View

Chapter IV

RESULTS AND DISCUSSION

The present investigation was intended to address the variation present in forty eight germplasm lines of finger millet. Genetic diversity was assessed at morphological level for facilitating their effective utilization in future hybridization programmes.

4 DIVERSITY ANALYSIS OF FINGER MILLET GENOTYPES USING MORPHOLOGICAL TRAITS

- 4.1 Mean performance of genotypes
- 4.2 Analysis of variance
- 4.3 Genetic variability, heritability and genetic advance.
- 4.4 Character association
- 4.5 Path coefficient analysis
- 4.6 Genetic divergence

4.1 Mean performance of genotypes

The mean values for 11 quantitative characters for 48 finger millet genotypes are given in Table 4.1. Performance of 4 qualitative characters for 48 genotypes is given in Table 4.2.

4.1.1 Quantitative characters

A. Plant height (cm)

Plant height ranged from 81.33 cm to 120.66 cm with a general mean of 103.33 cm. The shortest genotype was PR-202 (81.33 cm) while the tallest genotype was SRYA-333-SEL-2 (120.66 cm).

B. No of basal tillers per plant

The mean basal tillers per plant ranged from 3.77 tillers (PR-202) to 8.30 tillers (SRS-13447) with a general mean of 6.65 tillers per plant (Fig 2).

Table: 4.1 Mean values of the eleven quantitative characters in finger millet germplasm

S. No	Plant Height(cm)	No. of basal tillers/plant	No. of leaves on the main tiller	Productive tillers/Plant	Main ear length(cm)	Main ear width(cm)	Finger length(cm)	Finger width(cm)	Total fingers on the main ear	Grain yield /plant(g)	Grain yield/plot(g)
SNVD-11-5	106.88	7.52	22.55	7.10	8.41	6.16	7.96	1.05	7.99	33.29	1270.66
SNVD-11-15	113.10	6.11	19.2	4.766	7.05	5	6.73	1.03	6.33	20.19	598.33
snvd-11-28	109.21	5.55	19.33	5.13	7.59	4.62	6.26	1.08	6.13	16.69	789.33
SNVD-11-38	106.22	6.43	21.61	6.11	8.76	5.5	7.4	1.11	7.19	26.2	696.66
SNVD-11-41	107.21	7.45	23.01	7.31	7.59	6.33	8.23	1.08	7.11	34.69	874
SNVD-11-54	106.88	7.10	21.81	6.65	6.83	5.4	7.3	1.02	5.88	25.19	996
SNVD-11-72	102.88	7.46	22.33	7.4	10.82	6.16	8.23	0.99	6.44	34.67	1140.33
SNVD-11-77	102.77	7.56	21.33	7.56	10.66	6.56	8.46	1.03	8.66	37.25	1169
GPU-67	93.22	7.2	20.58	7.16	7.44	6.33	8.26	1.08	7.55	35.22	1258
SNVD-11-88	106.33	7.01	21.10	6.23	7.12	4.96	6.5	1.04	7.33	17.82	903
SNVD-11-89	95.10	6.81	23.10	5.66	7.19	5.1	6.9	1.07	7.66	21.44	847.66
SNVD-11-99	99.44	6.46	23.67	6.1	9.66	5.2	7.03	1.06	5.66	22.72	790.33
SNVD-11-112	110.44	7.46	22.71	7.46	7.88	6.3	8.33	1.14	7.66	36.27	1193
PR-202	81.33	3.77	25.88	3.77	8.07	5.13	6.96	1.08	6.33	22.43	536.33
AR-1	91.22	6.92	20.44	6.40	7.49	5.52	7.4	1.05	7.22	26.49	1251
SNVD-11-118	107.10	7.83	17.05	7.8	7.95	6.94	8.93	1.06	8.55	41.58	1162.66
AR-2	99.10	5.33	17.08	4.96	10.08	5.2	7.06	1.02	7.21	23.06	829.33
AR-3	106.33	6.77	21.27	5.1	7.04	5.13	7	1.05	6.77	22.76	1099
SRS-13466	104.55	7.56	19.31	7.36	9.89	6.44	8.2	0.99	9.99	35.92	1013
AR-4	90.11	6.54	25.55	6.54	8.38	6.1	8	1.11	7.33	32.58	889
AR-5	88.77	5.79	17.99	5.03	10.22	5.8	7.66	0.92	7.22	29.54	889
BAR-174	98.88	7.8	21.77	7.54	9.80	6.86	8.8	0.98	7.88	40.25	1269.33
CMLS-01-336-SEL-01	116.77	6.56	23.44	5.96	11.38	5.6	7.53	1.01	6.66	27.69	1183.66
CMLS-01-336-SEL-03	108.29	7.44	23.88	5.46	12.49	5.3	7.16	1.01	6.11	24.03	1225.33

CMLS-01-336-SEL-06	111.44	6.33	23.88	6.12	17.61	5	11.1	0.75	8.45	20.57	832.66
CMLS-01-336-SEL-07	101.33	6.63	22.55	6.1	17.44	5.16	11.63	0.87	7.44	22.69	867
CMLS-01-336-SEL-08	95.33	6.44	23.55	5.99	21.82	4.83	10.83	0.82	6.88	18.51	886
CMLS-01-336-SEL-09	101	6.88	24	6.6	17.82	5.36	12.06	0.74	7.23	24.98	734
Gpu-45	97.22	7.6	23.88	7.56	9.27	6.73	8.94	1.12	8.88	38.60	1100.33
CMLS-01-336-SEL-11	108.62	6.5	23.88	5.88	17.65	13.43	13.23	0.84	7.88	28.84	817.66
CMLS-01-336-SEL-12	112.33	5.03	25.55	4.83	17.39	10.80	10.16	0.83	6.87	15.76	1048
NSS-7928-SEL-1	106.10	7	21.95	6.96	7.83	6.2	8.1	1.16	6.99	33.45	1591.66
NSS-7928-SEL-2	99.88	5.44	21.11	5.21	7.16	5.33	6.96	1.11	7.55	24.34	1518.66
NSS-7928-SEL-3	105.33	6.55	23.33	6.33	7.60	5.73	7.29	1.06	7.77	28.62	1108.66
NSS-7928-SEL-4	103.74	4.76	23.10	4.55	7.97	4.9	6.7	1.09	7.44	19.48	1023.66
PSR-10095-SEL-1	103.10	6.17	21.55	6.07	8.72	5.86	7.76	0.97	9.44	30.23	1103.33
PSR-10121	93.22	5.5	22.44	4.2	8.5	4.63	6.93	0.98	8.11	16.83	657.33
SRYA-333-SEL-1	119.44	6.3	21.11	6.1	9	5.3	7.2	1.04	7.99	24.62	1085
SRYA-333-SEL-2	120.66	7.55	23.44	7.52	16.92	6.33	8.4	1.07	8.55	36.60	1153.66
SRYA-333-SEL-3	115.99	6.99	22.44	6.043	9.77	5.3	7.16	1.07	8.33	24.01	1348.66
SRS-13426	112.44	7.33	19.11	6.88	9.52	6.53	7.93	1.07	8.33	31.76	1121.66
SRS-13433	94.33	7.38	17.88	7	12.05	6.26	7.9	0.92	10.66	31.31	1061
SRS-13434	113.22	6.9	17.88	6.83	9.34	5.96	7.86	1.12	10.10	30.89	1303.66
SRS-13435	101.27	6.76	17.99	6.4	9.32	5.92	7.46	1.14	10.66	26.88	888.66
SRS-13436	111.88	7.1	18.33	6.36	9.5	5.76	7.46	1.23	9.33	26.37	922.66
SRS-13448	87.66	5.44	16.33	5.18	8.40	4.6	5.45	1.08	10.10	15.88	545.66
SRS-13439	95.11	5.82	16.55	4.96	8.71	5.10	6.76	1.06	10.60	19.83	817.66
SRS-13447	96.99	8.30	18.18	7	11.71	6.26	7.9	0.94	10.54	31.31	1069.33
Mean	103.33	6.65	21.37	6.19	10.22	5.93	8.03	1.02	7.89	27.30	1010.01
C.V	5.45	9.38	7.25	9.84	10.22	6.09	9.27	5.95	8.40	13.51	12.52
S.E	3.25	0.36	0.89	0.35	0.60	0.20	0.43	0.03	0.38	2.13	73.01
C.D 5%	9.14	1.01	2.51	0.98	1.69	0.58	1.20	0.09	1.07	5.98	205.02
C.D 1%	12.10	1.33	3.32	1.30	2.24	0.77	1.60	0.13	1.42	7.92	271.48



Fig: 2. Diversity in Basal Tillers



Fig: 3. Diversity in Ear Head

C. No. of leaves on the main tiller

The average number of leaves on the main tiller ranges from 16.33 to 25.88 with a general mean of 21.37. The data revealed that SRS-13448 (16.33) recorded minimum no. of leaves and maximum no. of leaves was found in genotype PR-202 (25.88).

D. Productive tillers per plant

The mean productive tillers per plant ranged from 3.77 tillers (PR-202) to 7.8 tillers (SNVD-11-118) with a general mean of 6.19 tillers per plant.

E. Main ear length (cm)

The average ear length recorded was 10.22 cm, with a range of 6.83 cm to 21.82 cm. The genotype SNVD-11-54 (6.83 cm) recorded the lowest length whereas; CMLS-01-336-SEL-08 (21.82 cm) had the highest ear length (Fig 3).

F. Main ear width (cm)

Ear width ranged from 4.6 cm to 13.43 cm with a general mean of 5.93 cm. The highest ear width was recorded for the genotype CMLS-01-11-SEL-11 (13.43) while the lowest was recorded for the genotype SRS 13448 (4.6 cm).

G. Finger length (cm)

The average length of finger recorded was 8.03 cm, with a range of 5.45 cm to 13.23 cm. The genotypes SRS-13448 (5.45 cm) recorded the lowest length whereas CMLS-01-336-SEL-11(13.23) had the highest finger length.

H. Finger width (cm)

Finger width ranged from 0.74 cm to 1.23 cm with a general mean 1.02 cm. The highest finger width was recorded for the genotype SRS-13436 (1.23 CM) while the lowest was recorded for the genotype CMLS-01-336-SEL-09 (0.74 cm).

I. Total fingers on the main ear

The mean values for number of fingers ranged from 5.66 (SNVD-11-99) to 10.66 (SRS-13433, SRS-13435) with general mean 7.89.



Fig: 4. Nodal Pigmentation



Fig: 5. Plant Lodging

J. Grain yield per plant (g)

The mean for grain yield per plant was 27.30g and the mean value ranged from 15.76g to 41.58g. The genotype CMLS-01-336-SEL-12 recorded lowest grain yield per plant where the genotype SNVD-11-118 exhibited highest grain yield per plant.

K. Grain yield per plot (g)

The mean grain yield per plot recorded 1010.01 g and the mean values ranged from 536.33 g (PR-202) to 1591.66 g (NSS-7928-SEL-1). Among the genotypes tested NSS-7928-SEL-1 recorded the highest grain yield per plot and PR-202 recorded the lowest grain yield per plot.

Among the 48 genotypes SNVD-11-118 which recorded highest mean grain yield per plant also possessed the maximum mean value for total productive tillers, thus the SNVD-11-118 could be used as a promising donor for these two characters. Genotype CMLS-01-336-SEL-11 was recorded highest mean value for ear width and finger length, SRYA-333-SEL-2 recorded highest plant height, PR-202 for maximum no. of leaves, CMLS-01-336-SEL-08 for maximum main ear length, SRS-13436 for highest finger width, SRS-13433 and SRS-13435 for maximum no. of finger and NSS-7928-SEL-1 for grain yield per plot. The above mentioned genotypes will be useful for increased productivity.

4.1.2 Qualitative characters

L. Nodal pigmentation

Among all 48 genotypes 17 genotypes showed the presence of pigmentation. Other 31 genotypes showed lack of pigmentation (Fig 4).

M. Degree of lodging at maturity

Out of 48 genotypes 32 genotypes were highly susceptible to lodging, 13 genotypes were intermediate to lodging and remaining 3 genotypes showed lower reaction to lodging (Fig 5).

N. Senescence/ stay green colour at maturity

Among the 48 genotypes 13 genotypes showed presence of senescence, remaining 35 genotypes showed lack of senescence

O. Grain colour

Out of 48 genotypes 22 genotypes were having light brown colour, 21 genotypes were having copper brown colour and remaining 5 were purple brown colour

4.2 ANALYSIS OF VARIANCE

Analysis of variance for the experiment involving a set of 48 finger millet genotypes for 11 quantitative characters viz., plant height (cm), no. of basal tillers per plant, no. of leaves on the main tiller, productive tiller per plant, main ear length (cm), main ear width (cm), finger length (cm), finger width (cm), total no of finger on the main ear, grain yield per plant (g) and grain yield per plot (g), revealed that the mean sum of squares were highly significant for all the characters indicating greater diversity among the 48 finger millet genotypes studied (Table 4.3).

4.3 GENETIC VARIABILITY, HERITABILITY AND GENETIC ADVANCE

The genotypic and phenotypic coefficients of variation, heritability and genetic advance as per cent of mean were estimated for 48 genotypes. Results are furnished in Table 4.4 for PCV, GCV and heritability, genetic advance as percent of mean respectively. The characters studied in the present investigation exhibited low, moderate and high PCV and GCV values.

A. Plant height (cm)

The genotypic and phenotypic coefficients of variation estimates observed for this trait were low i.e., 7.77 and 9.50, respectively. The observed heritability estimates for this character was high (67) with medium genetic advance as per cent of mean (13.11). The similar result reported by John (2002) for low GCV and PCV, high heritability and medium genetic advance as percent of mean, Prabhu *et al.* (2008) for low PCV, GCV and high heritability.

B. No. of basal tillers per plant

The genotypic and phenotypic coefficients of variation for this trait were medium i.e., 12.48 and 15.61 respectively. The observed heritability estimate was high (63) and with

Table: 4.2 Scoring of forty eight finger millet germplasm for four qualitative characters.

S.NO	Genotypes	Nodal pigmentation (0 absent/1 present)	Degree of lodging at maturity (3high/5intermedi ate/7 low)	Senescence/stay green colour(0 absent/1 present)	Grain colour (1 white/2 light brown/3 copper brown/4 purple brown/	Grain yield /plant (g)	Grain yield/plot (g)
1	SNVD-11-5	1	3	0	2	33.29	1270.66
2	SNVD-11-15	1	3	0	3	20.19	598.33
3	snvd-11-28	0	3	0	2	16.69	789.33
4	SNVD-11-38	0	3	0	3	26.2	696.66
5	SNVD-11-41	0	7	1	2	34.69	874
6	SNVD-11-54	0	5	1	3	25.19	996
7	SNVD-11-72	1	7	0	2	34.67	1140.33
8	SNVD-11-77	0	3	0	2	37.25	1169
9	GPU-67	0	3	0	2	35.22	1258
10	SNVD-11-88	1	3	1	4	17.82	903
11	SNVD-11-89	1	5	1	3	21.44	847.66
12	SNVD-11-99	1	3	0	3	22.72	790.33
13	SNVD-11-112	0	3	0	3	36.27	1193
14	PR-202	0	5	0	3	22.43	536.33
15	AR-1	0	3	0	3	26.49	1251
16	SNVD-11-118	1	5	0	2	41.58	1162.66

17	AR-2	0	3	0	3	23.06	829.33
18	AR-3	0	5	1	3	22.76	1099
19	VL-149	1	3	0	2	35.92	1013
20	AR-4	1	3	0	3	32.58	889
21	AR-5	1	7	1	3	29.54	889
22	BAR-174	1	5	1	2	40.25	1269.33
23	CMLS-01-336-SEL-01	1	3	0	3	27.69	1183.66
24	CMLS-01-336-SEL-03	1	5	1	4	24.03	1225.33
25	CMLS-01-336-SEL-06	0	3	1	3	20.57	832.66
26	CMLS-01-336-SEL-07	0	3	1	2	22.69	867
27	CMLS-01-336-SEL-08	1	3	0	2	18.51	886
28	CMLS-01-336-SEL-09	0	3	0	2	24.98	734
29	GPU-45	1	3	0	2	38.60	1100.33
30	CMLS-01336-SEL-11	0	5	0	2	28.84	817.66
31	CMLS-01-336-SEL-12	0	3	0	3	15.76	1048
32	NSS-7928-SEL-1	0	3	0	3	33.45	1591.66
33	NSS-7928-SEL-2	0	3	0	2	24.34	1518.66
34	NSS-7928-SEL-3	0	3	0	2	28.62	1108.66
35	NSS-7928-SEL-4	0	3	0	2	19.48	1023.66
36	PSR-10095-SEL-1	1	3	1	3	30.23	1103.33
37	PSR-10121	0	5	1	2	16.83	657.33
38	SRYA-333-SEL-1	0	3	0	2	24.62	1085
39	SRYA-333-SEL-2	0	3	0	2	36.60	1153.66
40	SRYA-333-SEL-3	0	3	1	2	24.01	1348.66

41	SRS-13426	0	5	0	4	31.76	1121.66
42	SRS-13433	0	3	0	4	31.31	1061
43	SRS-13434	1	5	0	2	30.89	1303.66
44	SRS-13435	0	3	0	4	26.88	888.66
45	SRS-13436	0	3	0	3	26.37	922.66
46	VR-708	0	5	0	3	15.88	545.66
47	SRS-13439	0	3	0	3	19.83	817.66
48	SRS-13447	0	5	0	3	31.31	1069.33

Table: 4.3 The mean sum of squares for all the 11 characters in finger millet germplasm

S.No.	Characters	Replication df:2	Genotypes df;47	Error df:94
1	Plant height(cm)	4.709	225.538 **	31.808
2	No of basal tillers/plant	1.417 *	2.459 **	0.389
3	No of leaves on the main tiller	9.298 *	19.112 **	2.402
4	Productive tillers/Plant	1.398 *	3.000 **	0.372
5	Main ear length(cm)	1.037	38.962 **	1.095
6	Main ear width(cm)	0.765 **	6.494 **	0.131
7	Finger length(cm)	1.613	7.092 **	0.556
8	Finger width(cm)	0.001	0.032 **	0.004
9	Total no of fingers on the main ear	0.677	5.350 **	0.441
10	Grain yield/plant(g)	66.833 **	143.654 **	13.614
11	Grain yield/plot(g)	95248.170 **	1 65736.900 **	15993.470

**** Significant at 1% probability level * Significant at 5% probability level**

high genetic advance as per cent of mean (20.56). The similar results reported by Mohan Prem Anand *et al.* (2005) for high heritability coupled with genetic advance as percent of mean, Sameer Kumar (1995) reported for medium PCV and GCV.

C. No. of leaves on the main tiller

The genotypic and phenotypic coefficients of variation for this trait were medium i.e., 11.04 and 13.20 respectively. The observed heritability estimate was high (69) and with medium genetic advance as per cent of mean (19). The similar results reported by Mohan Prem Anand *et al.* (2005) for medium PCV, GCV, high heritability and medium genetic advance as percent of mean.

D. Productive tillers per plant

A medium GCV (15.10) and PCV (18.03) were observed for this trait. The heritability estimates for this trait was high (70) coupled with high genetic advance as per cent of mean (26.07). The similar results were observed by Sonnad *et al.* (2008) and Priyadharshini *et al.* (2011) for high heritability coupled with high genetic advance as percent of mean, Kumar (1995) reported for medium PCV and GCV

E. Main ear length (cm)

The GCV and PCV for this trait were high i.e., 34.73 and 36.20 respectively. The heritability observed for this trait was high (92). This character recorded high genetic advance as per cent of mean (68). The similar results were observed by Jain and Yadava (1999) and Kumar (1995) for high heritability and genetic advance as percent of mean, Jain and Yadava (1999) reported high PCV.

F. Main ear width (cm)

The GCV and PCV for this trait were high i.e., 24.52 and 25.26, respectively. The heritability observed for this trait was high (94). This character recorded high genetic advance as per cent of mean (49.02). Supportive evidence for this character is not available.

G. Finger length (cm)

A medium GCV (18.73) and high PCV (20.58) were observed for this trait. The heritability estimate for this trait was high (79) with high genetic advance as per cent of mean (33.78). The similar results were observed by Lal *et al* (1996) for high PCV, heritability and genetic advance as percent of mean. Sonnad *et al.* (2008) reported medium GCV for this character.

H. Finger width (cm)

A low GCV (9.45) and medium PCV (11.17) were observed for this trait. The heritability estimate for this trait was high (71) with medium genetic advance as per cent of mean (16.46). The similar results were observed by Bendale *et al* (2002) for low GCV.

I. Total no fingers on the main ear

A medium GCV (16.19) and PCV (18.24) were observed for this trait. The heritability estimate for this trait was high (78) with high genetic advance as per cent of mean (29.60). The similar results were observed by Prabhu *et al.* (2008) and Mohan Prem Anand *et al.* (2005) for medium PCV, GCV and high heritability coupled with high genetic advance as percent of mean.

J. Grain yield per plant (g)

A high genotypic coefficient of variation (24.11) and phenotypic coefficient of variation (27.64) were observed for this trait. A high heritability estimate (76) coupled with high genetic advance as per cent of mean (43.33) recorded for this character. The results are conformity with Lal *et al.* (1996), Prabhu *et al.* (2008) and Mohan Prem Anand *et al.* (2005) for high GCV and PCV and high heritability coupled with high genetic advance as percent of mean.

K. Grain yield per plot (g)

A high genotypic coefficient of variation (22.12) and phenotypic coefficient of variation (25.41) were observed for this trait. A high heritability estimate (75) coupled with high genetic advance as per cent of mean (39.65) recorded for this trait.

The knowledge of genetic variability present in a given crop species for the character under improvement is of paramount importance for the success of any plant breeding programme. Information on coefficient of variation is useful in measuring the range of variability present in the characters. Heritability and genetic advance are important selection parameters. Genotypic coefficient of variation (GCV) along with heritable estimates would provide a better picture of the amount of genetic advance to be expected by phenotypic selection (Burton, 1952). It is suggested that genetic gain should be considered in conjunction with heritability estimates (Johnson *et al.*, 1955). Heritability estimates along with genetic advance are normally more helpful in predicting the gain under selection than heritability estimates alone.

Coefficients of variation studies indicated that the estimates of PCV were slightly higher than the corresponding GCV estimates for all the characters, indicating that the characters were less influenced by the environment. Therefore, selection on the basis of phenotype alone can be effective for the improvement of these traits.

The estimates of heritability act as predictive instrument in expressing the reliability of phenotypic value. Therefore, high heritability helps in effective selection for a particular character. Heritability in broad sense is the ratio of genotypic variance to the phenotypic variance and is expressed in percentage. In the present study all quantitative characters show high heritability (broad sense). High heritability for quantitative characters indicates the scope of genetic improvement of these characters through selection.

If the value of heritability in broad sense is high, it indicates that though the character is least influenced by the environmental effects, the selection for improvement of

Table: 4.4 Estimation of variability, heritability and genetic advance as per cent of mean for eleven characters in 48 genotypes

SL.No	Character	Variance		GCV (%)	PCV (%)	h ² (%) (Broad sense)	GA	GA as percent of mean (5%)
		Genotypic	Phenotypic					
1	Plant height(cm)	64.57	96.38	7.77	9.50	67	13.55	13.11
2	No of basal tillers/plant	0.69	1.07	12.48	15.61	63	1.36	20.56
3	No of leaves on the main tiller	5.57	7.97	11.04	13.20	69	4.06	19
4	productive tillers/Plant	0.87	1.24	15.10	18.03	70	1.61	26.07
5	Main ear length(cm)	12.62	13.71	34.73	36.20	92	7.02	68.63
6	Main ear width(cm)	2.12	2.25	24.52	25.26	94	2.91	49.02
7	Finger length(cm)	2.17	2.73	18.37	20.58	79	2.71	33.78
8	Finger width(cm)	0.009	0.01	9.45	11.17	71	0.16	16.46
9	Total no of fingers on the main ear	1.63	2.07	16.19	18.24	78	2.33	29.60
10	Grain yield/plant(g)	43.34	56.96	24.11	27.64	76	11.83	43.33
11	Grain yield/plot(g)	49914.48	65907.95	22.12	25.41	75	400.52	39.65

such character sometimes may not be useful, because broad sense heritability is based on total genetic variance which includes both fixable (additive) and nonfixable (dominance and epistasis) variances. On the other hand if the value of genetic advance is high, it shows that the character is governed by additive genes and selection will be rewarding for improvement of such trait.

So high heritability accompanied with high genetic advance indicates most likely the heritability is due to additive gene effect and selection may be effective.

In the present investigation, high heritability coupled with high genetic advance as per cent of mean was observed for no. of basal tillers per plant, no. of productive tillers per plant, main ear length, main ear width, finger length, total no. of fingers on the main ear, grain yield per plant and grain yield per plot. Thus, these traits are predominantly under the control of additive gene action and hence these characters can be improved by selection.

High heritability with moderate genetic advance was recorded for plant height, no. of leaves on the main tiller and finger width. These traits appear to be under the control of both additive and non-additive gene actions.

L. Variability in qualitative characters

Qualitative characters are useful criteria for characterization of germplasm accessions, as they show high heritability and stable expression. Further, if qualitative characters show association with yield components, it can serve as a marker in selection process. The variability for four qualitative characters viz., nodal pigmentation, degree of lodging at maturity, senescence and grain colour present in national collection of finger millet accession are discussed here.

Four characters have given code to describe their form of appearance which were presented in Table 4.5. Nodal pigmentation is given code no. (0 absent/1 present), degree of lodging is given code no. (3 high/5 intermediate/7 low), senescence/ stay green colour is given code no. (0 absent/1 present) and grain colour is given code no. (1 white/2 light brown/3 copper brown/4 purple brown). Scoring was done on the basis of coding and the following result was recorded viz., out of 48 genotypes 17 genotypes showing presence of nodal pigmentation and 31 genotypes showing absence of nodal pigmentation, out of 48

genotypes 32 genotypes showed high susceptibility to lodging, 13 genotypes showed intermediate reaction to susceptibility and remaining 3 genotypes showed low susceptibility to lodging, out of forty eight genotypes 13 showed presence of green colour at maturity and 35 showed absence of green colour at maturity. 22 genotypes were recorded light green grain colour, 21 copper brown colour and 5 with purple brown colour, whereas no genotype was recorded with white colour.

Highest yield per plant was observed for the genotype SNVD-11-118 and was showing presence of nodal pigmentation and lowest yield for the genotypes CMLS-01-336-SEL-12 showing absence of nodal pigmentation. It has been clear from the result that most of the lines having high yield showed presence of nodal pigmentation. Some lines which is having low yield also showed presence of pigmentation. The genotype SNVD-11-118 having higher grain yield showed presence of light brown grain colour. It has been recorded that the genotypes having intermediate lodging and lack of senescence counted higher yielding. The results are conformity with Shigeta (1985), Sripichitt *et al.* (2007) and Vadivoo *et al.* (1998).

The appearance of these characters is shown in frequency reveals that there is a huge variation in the appearance of these characters, which are presented in table 4.5. In case of nodal pigmentation genotypes without nodal pigmentation is more with 64.58% frequency and genotypes with pigment is less with 35.41%. Genotypes with higher susceptibility to lodging recorded higher in number among 48 genotypes with 66.66% frequency, genotypes with intermediate lodging having less genotypes than susceptible one with 27.08% frequency, genotypes with green colour at maturity is less in no. with 27.08% frequency and genotypes without senescence recorded 72.91%. Genotypes having grain colour light brown occurred with 45.83% frequency, copper brown with 43.7% frequency and purple brown with 10.41% frequency. The results are conformity with Sripichitt *et al.* (2007).

4.4 CHARACTER ASSOCIATION

Crop yield is the end product of the interaction of a number of other, often interrelated attributes. A thorough understanding of the interaction of characters among themselves had been of great use in plant breeding. The efficiency of selection for yield mainly depends on the direction and magnitude of association between yield and its component characters and also among themselves. Character association provides information on the nature and extent of association between pairs of metric traits and helps in selection for the improvement of the character. Phenotypic and genotypic correlations

were worked out on yield and yield contributing characters in 48 genotypes. In general, most of genotypic correlations were found to be higher than phenotypic correlations, which indicate that though there is strong inherent association between character studies, its expression is lessened due to influence of environment (Table 4.6).

component characters and also among themselves. Character association provides information on the nature and extent of association between pairs of metric traits and helps in selection for the improvement of the character. Phenotypic and genotypic correlations were worked out on yield and yield contributing characters in 48 genotypes. In general, most of genotypic correlations were found to be higher than phenotypic correlations, which indicate that though there is strong inherent association between character studies, its expression is lessened due to influence of environment (Table 4.6).

A. Plant height (cm)

Plant height recorded a significant positive correlation with no. of basal tillers per plant (0.216P, 0.3463G), no. of productive tillers per plant (0.2117P, 0.2761G), main ear width (0.1724P, 0.2093G), grain yield per plot (0.2495P, 0.3876G) at both genotypic and phenotypic levels, positive and non-significant correlation with no. of leaves on the main tiller (0.0432P, 0.1093G), finger width (0.0498P, 0.0409G), grain yield per plant (0.0719P, 0.1042G), finger length (0.0910P, 0.1445G) at both levels, positive and non-significant with main ear length (0.1092) at phenotypic level and positive significant (0.1666) at genotypic level. Negative correlation was recorded with finger no on the main ear.

The similar results were reported by Ravikumar and Seetharam (1993) for basal tillers per plant, productive tillers per plant, grain yield per plant, Sonnad *et al.* (2008) for positive main ear length, negative total finger on the main ear, Bedis *et al.* (2006) for grain yield per plot, positive significant main ear length, Bendale *et al.* (2002) for finger length.

B. No. of basal tillers per plant

No. of basal tillers per plant recorded a significant positive correlation with productive tillers per plant (0.8332P, 0.9271G), with grain yield per plant (0.6814P, 0.7230G), grain yield per plot (0.4181P, 0.5167G), finger length (0.2289P, 0.1973G) and total finger on the main ear (0.2545P, 0.2524G) at both levels, negative and non-significant

Table: 4.5 Frequency at which qualitative characters occurs

Character	Code no.	Description	Percentage frequencies of each character
Nodal pigmentation	0	Absent	64.58
	1	present	35.41
Degree of lodging at maturity	3	high	66.66
	5	intermediate	27.08
	7	low	6.25
Senescence/ stay green colour	0	Absent	72.91
	1	Present	27.08
Grain colour	1	White	Nil
	2	Light brown	45.83
	3	Copper brown	43.75
	4	Purple brown	10.41

correlations were recorded for no of leaves on the main tiller (-0.0753P, -0.1400G), positive non-significant correlation with main ear length (0.0260P, 0.0379G) and finger width (0.0502P, 0.0628G) at both levels. The similar results were reported by Sonnad *et al.* (2005) for finger length and ear length, Ravikumar and Seetharam (1993) for productive tillers per plant, Kumar (1995) for grain yield per plant, Bendale *et al.* (2002) for finger width.

C. No. of leaves on the main tiller

No. of leaves on the main tiller recorded a significant positive correlation with main ear length (0.2653P, 0.3606G), main ear width (0.1808P, 0.2166G), finger length (0.3315P, 0.4146G) at both levels, significant negative correlation recorded for finger no. (-0.4668P, -0.6214G) at both levels, negative and non-significant correlations were recorded for grain yield per plant (-0.0297P, -0.0541G), productive tillers per plant (-0.0208p, -0.0672g) at both levels.

The similar results were reported by Anantharaju and Minakshiganesan (2005) for productive tillers per plant and finger length. Supportive evidence for other characters are not available.

D. Productive tillers per plant

Productive tillers per plant recorded a significant positive correlation with grain yield per plant (0.8249P, 0.8450G), ear width (0.2546P, 0.1914G), finger length (0.3048P, 0.2862G), finger no. on the main ear (0.2921P, 0.2673G), grain yield per plot (0.4830P, 0.5168G) at both phenotypic and genotypic levels, positive and non-significant correlation with main ear length (0.0520P, 0.00436G) and finger width (0.0844P, 0.1113G) at both genotypic and phenotypic levels.

The similar results were reported by Priyadharshini *et al.* (2011), Anantharaju Minakshiganesan (2005) and Kumar (1995) for grain yield per plant, Kumar (1995) ear length, Priyadharshini *et al.* (2011) for finger length, total finger on the main ear, Sonnad (2005) for finger length.

Table: 4.6 Phenotypic (P) and genotypic (G) correlation coefficients among yield and yield attributes in forty eight genotypes

S. No	Character		Plant height (cm)	No of basal tillers/plant	No of leaves on the main tiller	Productive tillers/Plant	Main ear length (cm)	Main ear width(cm)	Finger length(cm)	Finger width(cm)	Total fingers on the main ear	Grain yield /plot(g)	Grain yield/plant (g)
1	PH	P	1.0000	0.2166**	0.0432	0.2117*	0.1092	0.1724*	0.0910	0.0498	-0.0608	0.2495**	0.0719
		G	1.0000	0.3463**	0.1093	0.2761**	0.1666*	0.2093*	0.1445	0.0409	-0.0815	0.3876**	0.1042
2	NBT	P		1.0000	-0.0753	0.8332**	0.0260	0.1762*	0.2289**	0.0502	0.2545**	0.4181**	0.6814**
		G		1.0000	-0.1400	0.9271**	0.0379	0.1227	0.1973*	0.0628	0.2524**	0.5167**	0.7230**
3	NL	P			1.0000	-0.0208	0.2653**	0.1808*	0.3315**	-0.1583	-0.4668**	0.0445	-0.0297
		G			1.0000	-0.0672	0.3606**	0.2166**	0.4146**	-0.3088**	-0.6214**	0.0118	-0.0541
4	PT	P				1.0000	0.0520	0.2546**	0.3048**	0.0844	0.2921**	0.4830**	0.8249**
		G				1.0000	0.0436	0.1914*	0.2862**	0.1113	0.2673**	0.5168**	0.8450**
5	EL	P					1.0000	0.3332**	0.7170**	-0.6672**	0.0016	-0.1001	-0.1047
		G					1.0000	0.3590**	0.8495**	-0.8419**	0.0202	-0.1496	-0.1295
6	EW	P						1.0000	0.5588**	-0.2366**	0.0967	0.1658*	0.3500**
		G						1.0000	0.5902**	-0.2862**	0.0649	0.1387	0.2828**
7	FL	P							1.0000	-0.5916**	0.0269	0.0529	0.2422**
		G							1.0000	-0.7770**	-0.0483	-0.0336	0.1731*
8	FW	P								1.0000	0.0578	0.1855*	0.1922*
		G								1.0000	0.0974	0.2794**	0.2449**
9	TF	P									1.0000	0.0798	0.2664**
		G									1.0000	0.0578	0.2217**
10	GYP	P										1.0000	0.5230**
		G										1.0000	0.5371**
11	GYPP	P											1.0000
		G											1.0000

PH- Plant height(cm), NBT-No of basal tillers per plant, NL- No of leaves on the main tiller, PT- Productive tillers per plant, EL-Main ear length, EW-Main ear width, FL- finger length, FW- Finger width, TF-Total finger on the main ear, GYP-Grain yield per plot, GYPP- Grain yield per plant

E. Main ear length (cm)

Main ear length recorded a significant positive correlation with finger length (0.7170P, 0.8495G), ear width (0.3332P, 0.3590G), at both levels, significant negative correlation with finger width (-0.6672P, -0.8419G) at levels, negative and non-significant correlation were recorded for grain yield per plant (-0.1047P, -0.1295G), grain yield per plot (-0.1001P, -0.1496G) at both levels. The similar results were reported by Sonnad *et al.* (2008) for finger length and finger no, John (2006) for grain yield per plant.

F. Main ear width (cm)

Main ear width recorded significant positive correlation with grain yield per plant (0.3500P, 0.2828G) and finger length (0.5588P, 0.5902G) at both levels, significant negative correlation with finger width (-0.2366P, -0.2862G) at both levels, positive and non-significant correlation with finger no. (0.0967P, 0.0649G) at both levels.

G. Finger length (cm)

Finger length recorded a significant positive correlation with grain yield per plant (0.2422P, 0.1731G) at both levels, significant negative correlation with finger width (-0.5916P, -0.7770G) at both level, positive and non-significant correlation with grain yield per plot (0.0529P), total finger on the main ear (0.0269P) at phenotypic level, negative and non-significant correlation with grain yield per plot (-0.0336G), total finger on the main ear (-0.0483G) at genotypic level.

The similar results were reported by Sonnad *et al.* (2008) and Lal (1996) for grain yield per plant. Sonnad *et al.* (2008) also reported negative correlation with finger no at genotypic level, negative and non-significant correlation with finger width but here correlation with finger width is significantly negative.

H. Finger width (cm)

Finger width recorded a significant positive correlation with grain yield per plot (0.1855P, 0.2794G), grain yield per plant (0.1922P, 0.2449G) at both level, positive and non-significant correlation with total finger on the main ear (0.0578P, 0.0974G) at both level. The similar results were reported by Bendale et al. (2002) for grain yield per plant.

I. Total no of fingers on the main ear

Total fingers on the main ear recorded a significant positive correlation with grain yield per plant (0.2664P, 0.2217G) at both level. The similar results were reported by Ravikumar and Seetharam (1993) and Ravindran *et al.* (1996) at both levels.

J. Grain yield per plot (g)

Grain yield per plot recorded a significant positive correlation with grain yield per plant (0.5230P, 0.5371G) at both levels. Supportive evidence is not available.

M. Grain yield per plant (g)

Grain yield per plant recorded a significant positive correlation with no of basal tillers per plant (0.6814P, 0.7230G), productive tillers per plant (0.8249P, 0.8450G), main ear width (0.3500P, 0.2828G), finger length (0.2422P, 0.1731G), finger width (0.1922P, 0.2449G) total finger on the main ear (0.2664P, 0.2217G) and grain yield per plot (0.5230P, 0.5371G). Positive and non-significant correlation with plant height (0.0719P, 0.1042G), negative and non-significant correlation with no. of leaves on the main tiller (-0.0297P, -0.0541G) and main ear length (-0.1047P, -0.1295G).

Grain yield per plant showed positive significant association with no. of basal tillers, productive tillers, main ear width, finger length, finger width, total finger on the main ear and grain yield per plot. Similar kind of association was revealed by Kumar (1995) for no of basal tillers per plant, productive tillers, Sonnad *et al.* (2008) and Lal *et al.* (1996) for finger length, Ravindran *et al.* (1996) and Bedis *et al.* (2006) for total no. of fingers on the main year, finger width has been found positively significant in this experiment where as Bendale *et al.* (2002) recorded negative and non-significant correlation.

The result obtained indicated that, yield was increased whenever there was increase in basal tillers, no. of productive tillers, main ear width, finger length, finger width, total fingers on the main ear and grain yield per plot. Hence, these characters could be considered as criteria for selection for higher yield as these were mutually and directly associated with grain yield.

Grain yield per plant shows positive and non significant correlation with Plant height and negative non-significant correlation with no. of leaves and ear length. Similar kind of association was revealed by Priyadarshini *et al.* (2011), Sonnad *et al.* (2008), Anantharaju and Minakshiganesan (2005) for plant height, whereas Bedis *et al.* (2006) recorded significant positive correlation with plant height, John (2006) for ear length, where as

Sonnad *et al.* (2005) and Kumar (1995) recorded positive and non-significant correlation with main ear length. As plant height positively associated with grain yield it may consider for selection criteria for increase in grain yield.

4.5 PATH COEFFICIENT ANALYSIS

Correlation gives only the relation between two variables whereas path coefficient analysis allows separation of the direct effect and their indirect effects through other attributes by partitioning the correlations (Wright, 1921). Hence, this objective was undertaken in the present investigation.

Based on the data recorded on the genotypes in the present investigation, the genotypic and phenotypic correlations were estimated to determine direct and indirect effects of yield and yield contributing characters.

As discussed in character association based on the importance of phenotypic effects the present results of phenotypic and genotypic path coefficient of yield and yield contributing characters discussed here under which were presented in table 4.7 and Fig 4.6 and 4.7.

A. Plant height (cm)

Plant height had negative direct effect (-0.1394P, -0.1664G) on grain yield per plant at both phenotypic and genotypic levels, while the correlation of plant height with grain yield was positive and non-significant. The correlation with yield was positive due to positive indirect contribution through productive tillers per plant (0.1433P, 0.2799G), main ear width (0.0325P, 0.0406G), finger length (0.0134P, 0.0032G), grain yield per plot (0.0363P, 0.0566G). The similar results reported by Priyadarshini *et al.* (2011) and Bendale *et al.* (2002), Ravindran *et al.* (1996), Anantharaju and Meenakshiganesan (2005) negative direct effect of plant height on grain yield.

B. No. of basal tillers per plant

No. of basal tillers had positive phenotypic direct effect (0.0168P) and negative genotypic effect (-0.2540G) on grain yield per plant, while the correlation of no. of basal tillers with grain yield per plant was positive and significant at both levels. The correlation was positive and significant at both levels due to positive in direct effect by Productive tillers per plant (0.5637P, 0.9395G), main ear width (0.0332P, 0.0238G), finger length (0.0338P, 0.0044G), finger width (0.0054P, 0.0039G) and grain yield per plot (0.0608P, 0.0741G). The similar results reported by Lal *et al.* (1996), Sonnad *et al.* (2005) for positive phenotypic and negative genotypic effect on grain yield per plant.

C. No. of leaves on the main tiller

No. of leaves on the main tiller had negative direct effect (-0.0256P) on grain yield per plant at phenotypic level and direct positive effect (0.0079g) on grain yield per plant at genotypic level while the correlation between no. of leaves on the main tiller and grain yield per plant was negative and non-significant. This association mainly due to negative indirect effect influences through plant height (-0.0060P, -0.0182G), productive tillers per plant (-0.0141P, -0.0681G), main ear length (-0.0053P, -0.0552G), finger width (-0.0172P, -0.0194G) at phenotypic level and positive effect mainly due to positive indirect effect through main ear width (0.0341P, 0.0421G), finger length (0.0490P, 0.0092G) and grain yield per plot (0.065P, 0.0017G) at genotypic level. The similar results reported by Anantharaju and Meenakshiganesan (2005) and Dhanakod and Chandrasekharan (1989) for genotypic effects.

D. Productive tillers per plant

No. of productive tillers per plant had positive direct effect (0.6766P, 1.0134G) on grain yield per plant, on the other side productive tillers had positive and significant correlation with grain yield per plant. The correlation with grain yield per plant was positive due to positive indirect effect through main ear width (0.0480P, 0.0372G), finger length (0.0450P, 0.0064G), finger width (0.0092P, 0.0070G) and grain yield per plot (0.0703P, 0.0741G) on grain yield. The same result was reported by Kumar (1995), Ravikumar and Seetharam (1993), Bedis *et al.* (2006), Priyadarshini *et al.* (2011) and Anantharaju and Meenakshiganesan (2005) for positive direct effect on grain yield per plant.

E. Main ear length (cm)

Main ear length had negative direct effect (-0.2001P, -0.1531G) on grain yield per plant while correlation between main ear length and grain yield per plant was negative and non-significant. The correlation with grain yield per plant due to negative indirect effect through plant height (-0.0152P, -0.0277G), finger width (-0.0724P, -0.0529G), grain yield per plot (-0.0146P, -0.0214G). The same result reported by Kumar (1995) and Bedis *et al.* (2006) is negative direct effect of main ear length on grain yield per plant.

F. Main ear width (cm)

Main ear width had positive direct effect (0.1887P, 0.1941G) on grain yield per plant while correlation between main ear width and grain yield per plant was significantly positive. The correlation with grain yield is positive due to positive direct effect through

Productive tillers per plant (0.0.1722P, 0.1940G), finger length (0.0825P, 0.0131G), grain yield per plot (0.0241P, 0.0199G). Supportive evidence for main ear width is not available.

G. Finger length (cm)

Finger length had positive direct effect (0.1477P, 0.0222G) on grain yield per plant while correlation between finger length and grain yield per plant was significantly positive. The correlation with grain yield per plant was positive due to positive indirect effect through productive tillers (0.2062P, 0.0290G), main ear width (0.1055P, 0.1146G), total fingers on the main ear (0.0001P, 0.0008G). The same results reported by Sonnad *et al.* (2008), Anantharaju and Meenakshiganesan (2005), Lal *et al.* (1996) and Bendale *et al.* (2002) positive direct effect of finger length on grain yield per plant.

H. Finger width (cm)

Finger width had positive direct effect (0.0108P, 0.0628G) on grain yield per plant while correlation between finger width and grain yield per plant was significantly positive. The correlation with grain yield per plant was positive and significant due to the indirect positive effect through productive tillers per plant (0.0571P, 0.1128G) and main ear length (0.1335P, 0.1289G). The same result reported by Bendale *et al.* (2002) positive direct effect of finger width on grain yield per plant.

I. Total fingers on the main ear

Total fingers had phenotypic positive direct effect (0.0043P) and genotypic negative direct effect (-0.0165G) on grain yield per plant while the correlation between total finger on the main ear and grain yield was significantly positive. The correlation with grain yield per plant was positive and significant due to indirect positive effect through plant height (0.0085P, 0.0136G), productive tillers per plant (0.1976P, 0.2709G), main ear width (0.0182P, 0.0126G), finger width (0.0063P, 0.0061G), grain yield per plot (0.0116P, 0.0083G). The same result reported by Thakur and Saini (1995), Marimuthu (1997), Bendale *et al.* (2002) and Bedis *et al.* (2006) with grain yield per plant.

J. Grain yield per plot (g)

Grain yield per plot had positive direct effect (0.1455P, 0.1433G) on grain yield per plant while the correlation between grain yield per plot and grain yield per plant was positive significant. The correlation with grain yield per plant was positive and significant due to indirect positive effect through productive tillers per plant (0.3268P, 0.0.5238G), main ear length (0.0.0200P, 0.0229G), main ear width (0.0313P, 0.0269G), finger width (0.0201P, 0.0175G).

The association of different component characters among themselves and with yield is quite important for devising an efficient selection criterion for yield. The total correlation between yield and component characters may be some times misleading, as it might be an over-estimate or under-estimate because of its association with other characters. Hence, indirect selection by correlated response may not be some times fruitful. When many characters are affecting a given character, splitting the total correlation into direct and indirect effects of cause as devised by Wright (1921) would give more meaningful interpretation to the cause of association between the dependent variable like yield and independent variables like yield components. This kind of information will be helpful in formulating the selection criteria. Indicating the selection for these characters is likely to bring about an overall improvement in single plant yield directly.

As a guideline for interpretation of results of path analysis the following broad points may be kept in view (Singh and Chaudhary, 1977).

If the correlation coefficient between a causal factor and the effect is almost equal to its direct effect, then correlation explains the true relationship and a direct selection through this trait will be effective.

If the correlation coefficient is positive, but the direct effect is negative or negligible, the indirect effects seem to be the cause of positive correlation. In such situations, the indirect causal factors are to be considered simultaneously for selection.

Correlation coefficient may be negative but the direct effect is positive and high. Under these circumstances, a restricted simultaneous selection model is to be followed *i.e*

Table: 4.7 Phenotypic (P) and genotypic (G) path coefficient analysis indicating direct and indirect effects of components characters on grain yield

character		Plant height(cm)	No of basal tillers/plant	No of leaves on the main tiller	Productive tillers/plant	Main ear length(cm)	Main ear width(cm)	Finger length(cm)	Finger width (cm)	Total fingers on the main ear	Grain yield/plot (g)	Corelation
PH	P	-0.1394	0.0036	-0.0011	0.1433	-0.0219	0.0325	0.0134	0.0054	-0.0003	0.0363	0.0719
	G	-0.1664	-0.0880	0.0009	0.2799	-0.0255	0.0406	0.0032	0.0026	0.0013	0.0566	0.1042
NBT	P	-0.0302	0.0168	0.0019	0.5637	-0.0052	0.0332	0.0338	0.0054	0.0011	0.0608	0.6814**
	G	-0.0576	-0.2540	-0.0011	0.9395	-0.0058	0.0238	0.0044	0.0039	-0.0042	0.0741	0.7230**
NL	P	-0.0060	-0.0013	-0.0256	-0.0141	-0.00531	0.0341	0.0490	-0.0172	-0.0020	0.0065	-0.0297
	G	-0.0182	0.0356	0.0079	-0.0681	-0.0552	0.0421	0.0092	-0.0194	0.0103	0.0017	-0.0541
PT	P	-0.0295	0.0140	0.0005	0.6766	-0.0104	0.0480	0.0450	0.0092	0.0013	0.0703	0.8249**
	G	-0.0460	-0.2355	-0.0005	1.0134	-0.0067	0.0372	0.0064	0.0070	-0.0044	0.0741	0.8450**
EL	P	-0.0152	0.0004	-0.0068	0.0352	-0.2001	0.0629	0.1059	-0.0724	0.0000	-0.0146	-0.1047
	G	-0.0277	-0.0096	0.0029	0.0442	-0.1531	0.0697	0.0189	-0.0529	-0.0003	-0.0214	-0.1295
EW	P	-0.0240	0.0030	-0.0046	0.1722	-0.0667	0.1887	0.0825	-0.0257	0.0004	0.0241	0.3500**
	G	-0.0348	-0.0312	0.0017	0.1940	-0.0550	0.1941	0.0131	-0.0180	-0.0011	0.0199	0.2828**
FL	P	-0.0127	0.0038	-0.0085	0.2062	-0.1435	0.1055	0.1477	-0.0642	0.0001	0.0077	0.2422**
	G	-0.0240	-0.0501	0.0033	0.02900	-0.1301	0.1146	0.0222	-0.0488	0.0008	-0.0048	0.1731*
FW	P	-0.0069	0.0008	0.0040	0.0571	0.1335	-0.0446	-0.0874	0.01085	0.0003	0.0270	0.1922*
	G	-0.0068	-0.0159	-0.0025	0.1128	0.1289	-0.0556	-0.0173	0.0628	-0.0016	-0.0401	0.2449**
TF	P	0.0085	0.0043	0.119	0.1976	-0.0003	0.0182	0.0040	0.0063	0.0043	0.0116	0.2664**
	G	0.0136	-0.0641	-0.0049	0.2709	-0.0031	0.0126	-0.0011	0.0061	-0.0165	0.0083	0.2217**
GYP	P	-0.0348	0.0070	-0.0011	0.3268	0.0200	0.0313	0.0078	0.0201	0.0003	0.1455	0.5230**
	G	-0.0645	-0.1312	0.0001	0.5238	0.0229	0.0269	-0.0007	0.0175	-0.0010	0.1433	0.5371**

PH- Plant height(cm), NBT-No of basal tillers per plant, NL- No of leaves on the main tiller, PT- Productive tillers per plant, EL-Main ear length, EW-Main ear width, , FL- finger length , FW- Finger width, TF-Total finger on the main ear, GYP-Grain yield per plot,

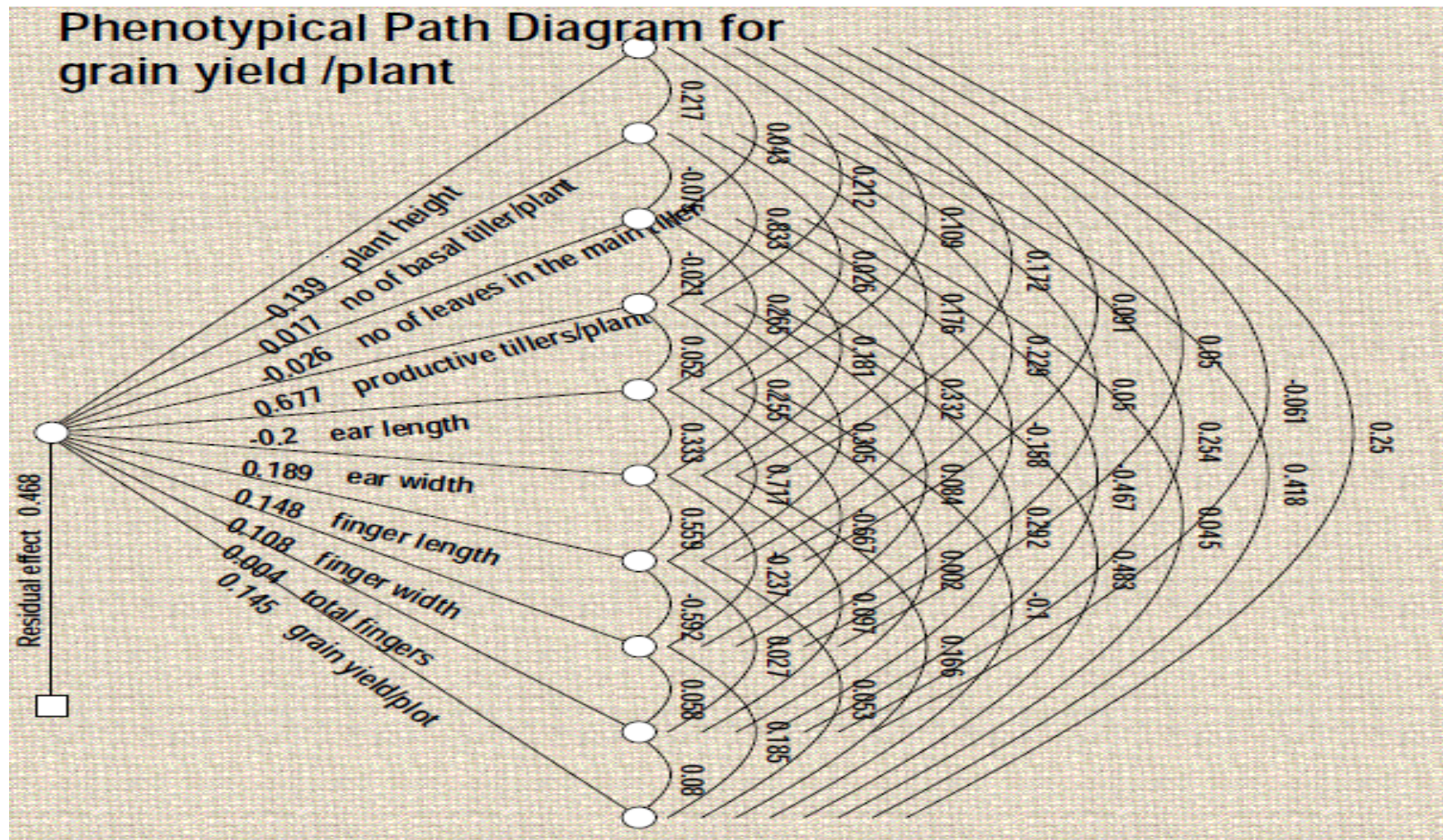


Fig:4.6 Phenotypical Path Diagram for grain yield /plant

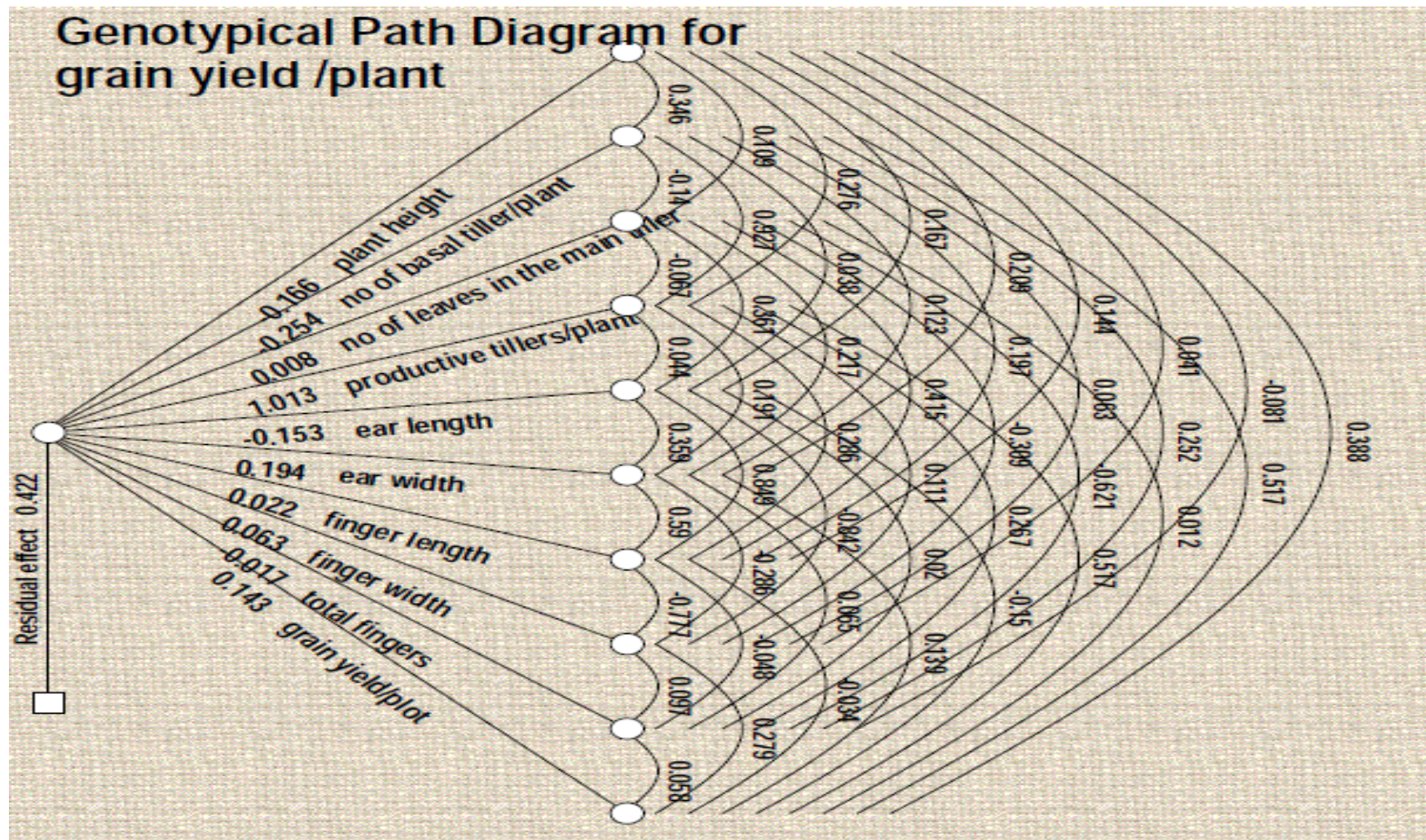


Fig: 4.7 Genotypical Path Diagram for grain yield /plant

restrictions are to be imposed to nullify the undesirable indirect effects in order to make use of the direct effect.

If correlation coefficient is negative and direct effect is also negative, then the selection based on that character has to be dropped.

The residual effect determines how best the causal factors account for the variability of the dependent factor. If the residual effect is high, some other factors which have not been considered here need to be included in this analysis to account fully for the variation in yield.

Path coefficient analysis revealed that number of productive tillers per plant exerted the highest positive direct effect on grain yield per plant, followed by main ear width, finger length, finger width and grain yield per plot along with significant positive correlation for all the above mentioned characters.

These characters also exhibited indirect positive effect viz., Productive tillers per plant exhibited indirect positive effect on grain yield through tillers main ear width, finger length, finger width and grain yield per plot, main ear width exhibited indirect positive effect through productive tillers per plant, finger length and grain yield per plot, finger length exhibited indirect positive effect through productive tillers, main ear width and total finger on the main ear, finger width exhibited indirect positive effect through productive tillers, main ear length, grain yield per plot exhibited indirect positive effect through productive tillers, main ear length, main ear width and finger width. The similar results were conformity with Ravindran *et al.* (1996) and Ravikumar and Seetharam (1993) for positive direct effect of productive tillers, Anantharaju and Meenakshiganesan (2005), Lal *et al.* (1996) for finger length, Bendale *et al.* (2002) for finger width.

Plant height had negative direct effect on grain yield per plant. Plant height exhibited indirect positive effect on grain yield through productive tillers main ear width finger length, finger width and grain yield per plot. Plant height recorded positive and non-significant correlation with grain yield per plant due to indirect positive effect through other characters. In such situations, the indirect causal factors are to be considered simultaneously for selection. The similar results were conformity with Bendale *et al.* (2002), Ravindran *et al.* (1996).

Main ear length had negative direct effect on grain yield per plant. Main ear length recorded negative and non-significant correlation with grain yield per plant. The similar results were conformity with Kumar (1995) and Bedis *et al.* (2006) negative direct effect of main ear length on grain yield per plant.

Path analysis revealed that number of productive tillers per plant, main ear width, finger length, finger width and grain yield per plot are the most important characters which could be used as selection criteria for effective improvement of grain yield.

4.6 GENETIC DIVERGENCE

The quantitative assessment of genetic divergence was made by adopting Mahalanobis D^2 statistic for yield and its contributing characters. Genetic divergence was estimated for 48 finger millet germplasm lines and the results obtained from the study are presented below.

4.4.1 Wilk's 'V' criterion test

Wilk's 'V' (statistic) criterion was used to test the significant differences between the groups based on the pooled effects of all the characters. The significance of 'V' (statistic) value was tested by % at 517 degrees of freedom. The 'V' statistic value was highly significant indicating that the genotypes differed significantly when all the characters were considered simultaneously.

The significance of 48 genotypes in the analysis of variance of dispersion clearly indicated the significant pooled effect of all the characters studied between different genotypes. Hence, further analysis was made to estimate D^2 analysis.

4.4.2 Mahalanobis's generalized distance D^2 values

The correlated unstandardized means of eleven quantitative characters studied were transformed to standardized uncorrelated set of variables by using pivotal condensation method. The statistical distance (Mahalanobis' D^2 value) between a pair of genotypes was obtained as sum of squares of differences between pairs of corresponding uncorrelated values of any two genotypes. These values were considered at a time and these were used for final grouping of genotypes.

4.4.3 Grouping of genotypes into various clusters

Forty eight genotypes were grouped into eight clusters based on D^2 values using Tocher's method (Rao, 1952) such that the genotypes belonging to same cluster had an average smaller D^2 values than those belonging to different clusters. The distribution of genotypes into various clusters is shown in Table 4.8 and Fig 4.8. Out of eight clusters, cluster I was the largest comprising of thirty three genotypes followed by clusters II with five genotypes, cluster IV with four genotypes, cluster VIII with two genotypes and clusters III, V, VI, VII with one genotype each. The clusters III, V, VI and VII were represented by single genotype indicating high degree of heterogeneity among the genotypes.

4.4.4 Average inter and intra cluster distances

Intra cluster D^2 values ranged from zero (cluster III, V, VI, VII) to 62.09 (cluster VIII). Maximum intra cluster distance was observed in cluster VIII (62.09), followed by cluster I (13.69), cluster II (10.95) and cluster IV (7.23). The intra cluster distance varied from a maximum 62.09 for cluster VIII to minimum 7.23 for cluster IV having 4 genotypes though it was zero for solitary clusters (III, V, VI, and VII) (Table 4.9). This reveals that genotypes occupying the same cluster have low level of diversity and selection of parents with in the cluster may not be considered promising as has been reported by Kumar *et al.* (2010).

From the inter cluster D^2 values of the eight clusters, it can be seen that the highest divergence occurred between cluster VI and VIII (1252.45), followed by cluster V and VIII (1235.52), cluster I and VIII (1224.30), cluster VII and VIII (1215.91), cluster III and VIII (1189.56), cluster IV and VIII (1160.76) and cluster II and VIII (1134.34).

The inter-cluster D^2 values were ranged widely with minimum value of 20.97 between clusters I and V and maximum value of 1252.45 between clusters VI and VIII indicating high diversity among the genotypes of these clusters. The maximum amount of heterosis is expected from the crosses with parents belonging to the most divergent clusters as has been reported by Kumar *et al.* (2010), Anantharaju and Meenakshiganesan (2008), and Kadam (2008). Hence, it is desirable to select the genotypes from the cluster showing

Table : 4.8 Cluster classification of finger millet germplasm (Tocher's method)

Cluster	Number of genotypes	Germplasms
I	33	SNVD-11-5,SNVD-11-15,SNVD-11-28,SNVD-11-38,SNVD-11-41, SNVD-11-54, SNVD-11-72, SNVD-11-77, GPU-67, SNVD-11-88, SNVD-11-89, SNVD-11-99, SNVD-11-112, AR-1, SNVD-11-118, AR-2, AR-3, SRS-13466, AR-4, AR-5, BAR-174, CMLS-01-336-SEL-01, GPU-45, NSS-7928-SEL-1, NSS-7928-SEL-3, NSS-7928-SEL-4,PSR-10095-SEL-1,PSR-10121, SRYA-333-SEL-1, SRYA-333-SEL-3, SRS-13426, SRS-13434, SRS-13436,
II	5	SRS-13433, SRS-13435, SRS-13448, SRS-13439, SRS-13447
III	1	CMLS-01-336-SEL-03
IV	4	CMLS-01-336-SEL-06, CMLS-01-336-SEL-07, CMLS-01-336-SEL-08, CMLS-01-336-SEL-09
V	1	NSS-7928-SEL-2,
VI	1	PR-202
VII	1	SRYA-333-SEL-2
VIII	2	CMLS-01-336-SEL-11, CMLS-01-336-SEL-12

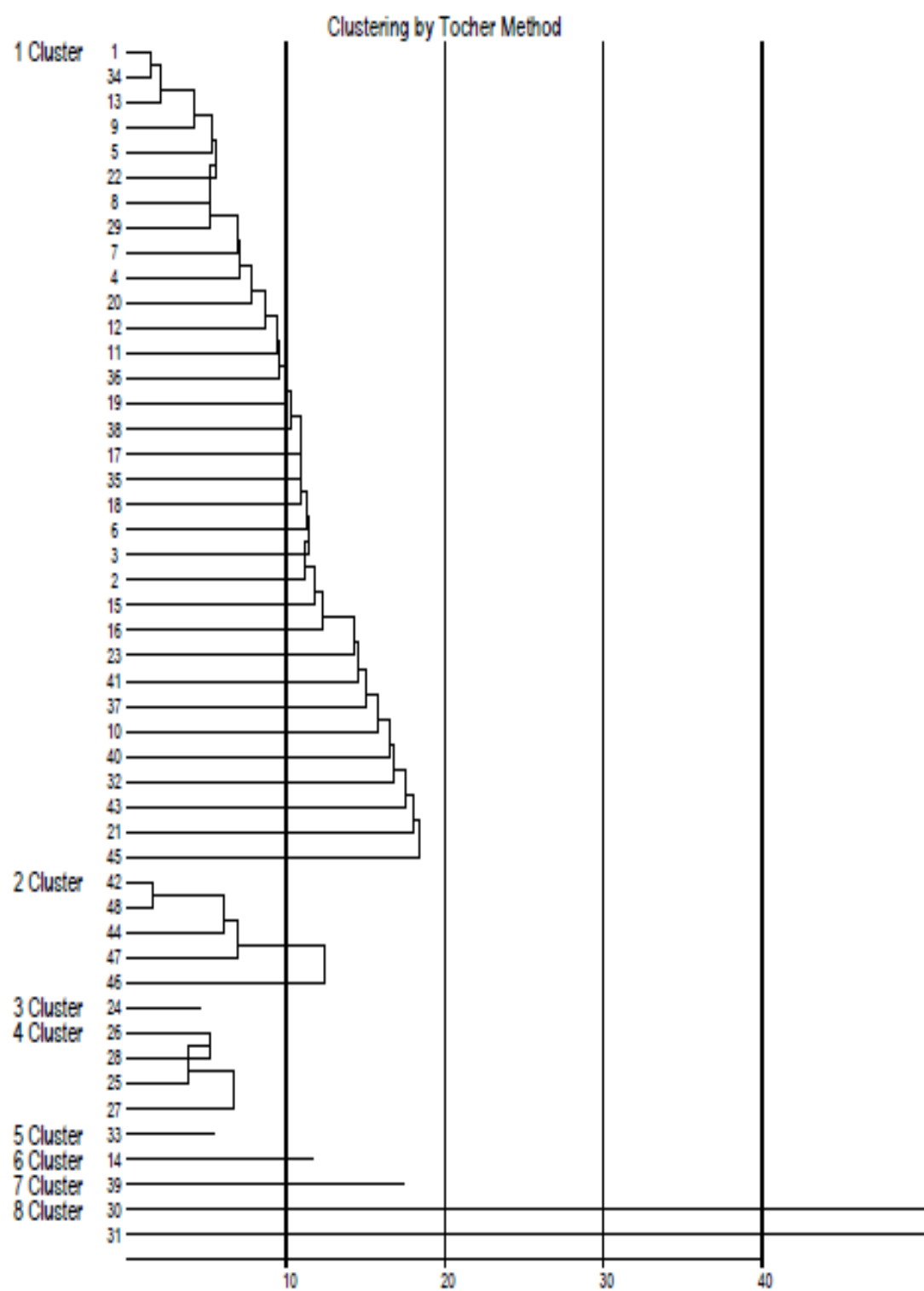


Fig: 4.8 Grouping of genotypes into various clusters

high inter-cluster distance in breeding programme for obtaining the desirable segregants.

The inter-cluster distances were higher than the intra-cluster distances indicating the presence of wider genetic diversity between the clusters rather than within the clusters.

4.4.5 Cluster means of the characters

The cluster means for each of eleven characters are presented in Table 4.10. From the data it can be seen that considerable differences existed for all the characters under study. The data indicated that the cluster mean for plant height was highest in cluster VII (120.66 cm) and the lowest in cluster VI (81.33 cm). No. of basal tillers per plant was highest in cluster VII (7.55) and lowest in cluster VI (3.77). No. of leaves on the main tiller was highest in cluster VI (25.88) and lowest in cluster II (17.39). A productive tiller per plant was highest in cluster VII (7.52) and lowest in cluster VI (3.77). Cluster IV recorded the highest main ear length (18.68 cm) and the lowest was recorded in the cluster V (7.16 cm). Main ear width was highest in cluster VIII (12.12 cm) and lowest in cluster IV (5.09 cm). Finger length was recorded highest in cluster VIII (11.70 cm) and lowest in cluster V (6.96 cm). Cluster V recorded highest finger width (1.12 cm) and the lowest was recorded in the cluster IV (0.80 cm). Total finger on the main ear was highest in cluster II (10.52) and lowest in cluster III (6.11). Grain yield per plant was highest in cluster VII (36.60) and lowest in cluster IV (21.69). Grain yield per plot was highest in cluster V (1518.67) and lowest in cluster II (876.47). The result indicates that selection of genotypes having high values for particular trait could be made and used in the hybridization programme for improvement of that character.

It is observed that no cluster contained at least one genotype with all the desirable traits, which ruled out the possibility of selecting directly one genotype for immediate use. Therefore, hybridization between the selected genotypes from divergent clusters is essential to judiciously combine all the targeted traits.

Genotype groups into cluster IV were low yielder for grain yields per plant associated with very low finger width and main ear width. Genotype groups in cluster VI were low grain yielder, low total no of basal tillers per plant, low total productive tillers per plant and low plant height. Higher yielder clusters are VII, I and II. Genotypes included in

Table: 4.9 Intra (diagonal) and inter clusters D value D^2 value and extant of diversity among the clusters

[illegible]

cluster VII is having highest mean value for grain yield per plant, total no of basal tillers per plant and total productive tillers per plant. Cluster II is having highest mean value for no of leaves on the main tiller and total fingers on the main ear. The genotypes SRYA-333-SEL-2 (VII) as this cluster had only one genotype which become automatic choice, BAR-174 and SNVD-11-118 (I), SRS-13447 and SRS-13433 (II) from these clusters having high mean values for grain yield per plant may be directly used for adaptation or may be used as parents in future hybridization programme as has been reported by Kumar *et al.* (2010) and Reddy *et al.* (1993).

4.4.6 Relative contribution of characters towards genetic divergence

The number of times that each of the eleven characters appeared in first rank and its respective per cent contribution towards genetic divergence is presented in Table 4.11. The results showed that the contribution of main ear length was highest towards genetic divergence (21.01%) by taking 237 times ranking first, followed by total fingers on the main ear (19.15%) by 216 times, grain yield per plot (16.84%) by 190 times, grain yield per plant (13.65%) by 154 times, main ear width (6.29%) by 71 times, total basal tillers per plant (5.59%) by 63 times, plant height (5.32%) by 60 times, no of leaves on the main tiller (4.34%) by 49 times, productive tillers per plant (4.08%) by 46 times, finger width (2.22%) by 25 times, finger length (1.51%) by 17 times respectively to the genetic divergence in decreasing order.

Among the 11 quantitative characters studied the most important character contributing to the divergence was main ear length followed by total no. of fingers on the main ear, grain yield per plot, grain yield per plant, main ear width, total no. of basal tillers per plant, no. of leaves on the main tiller, total productive tiller per plant, finger width, finger length. These results having conformity with Jaylal and Haider (1994), Kumar (1995), Anantharaju and Meenakshiganesan (2008).

TABLE: 4.10 Mean values of clusters for 11 characters in 48 finger millet germplasm (Tocher's method).

Cluster	Plant height (cm)	No of basal tillers/ plant	No of leaves on the main tiller	Productive tillers/Plant	Main ear length (cm)	Main ear width (cm)	Finger length (cm)	Finger width (cm)	Total fingers on the main ear	Grain yield/plant (g)	Grain yield/plot (g)
I	104.37	6.77	21.26	6.34	8.68	5.76	7.62	1.06	7.67	28.68	1044.82
II	95.07	6.74	17.39	6.11	10.04	5.63	7.10	1.03	10.52	25.05	876.47
III	108.29	7.44	23.89	5.47	12.50	5.30	7.17	1.01	6.11	24.03	1225.33
IV	102.28	6.57	23.50	6.20	18.68	5.09	11.41	0.80	7.50	21.69	829.92
V	99.89	5.44	21.11	5.21	7.16	5.33	6.96	1.12	7.55	24.35	1518.67
VI	81.33	3.77	25.88	3.77	8.08	5.13	6.97	1.09	6.33	22.43	536.33
VII	120.66	7.55	23.44	7.52	16.92	6.33	8.40	1.07	8.55	36.60	1153.67
VIII	110.48	5.77	24.72	5.36	17.52	12.12	11.70	0.84	7.38	22.30	932.83

Table: 4.11 Contribution of each 11 quantitative characters to the divergence

S.NO	CHARACTER	TIMES RANKED	CONTRIBUTION %
1	Plant height(cm)	60	5.32
2	No of basal tillers/plant	63	5.59
3	No of leaves on the main tiller	49	4.34
4	Productive tillers/ Plant	46	4.08
5	Main ear length(cm)	237	21.01
6	Main ear width(cm)	71	6.29
7	Finger length(cm)	17	1.51
8	Finger width(cm)	25	2.22
9	Total no of fingers on the main ear	216	19.15
10	Grain yield/plant(g)	154	13.65
11	Grain yield/plot(g)	190	16.84

In order to select genetically diverse genotypes the material should be screened for the important traits viz., main ear length, total no of fingers on the main ear, grain yield per plot, grain yield per plant, main ear width, total no of basal tillers per plant.

Chapter V

Summary and Conclusions

Chapter V

SUMMARY AND CONCLUSIONS

The present investigation was carried out at National Bureau of Plant Genetic Resources, Regional station, Rajendranagar during *kharif* 2012 with 48 finger millet germplasm lines to study the genetic variability, heritability, genetic advance as per cent of mean, character association path coefficient analysis and genetic divergence. The data was recorded on 15 characters *viz.*, plant height (cm), no. of basal tillers per plant, no. of leaves on the main tiller, no. of productive tillers per plant, main ear length (cm), main ear width (cm), finger length (cm), finger width (cm), total fingers on the main ear, grain yield per plant (g) and grain yield per plot (g) were subjected to statistical analysis for drawing valid conclusions.

The material chosen differed in their genotypic make up as evidenced by the significant differences among them in respect of all the quantitative characters studied. Phenotypic coefficient of variation estimates was slightly higher than the genotypic coefficient of variation for all the traits indicating low environmental influence on the expression of all the traits. A perusal of genetic parameters revealed that phenotypic coefficients of variation were high for main ear length, main ear width, finger length, grain yield per plant and grain yield per plot where as high genotypic coefficient of variation recorded for main ear length, main ear width, grain yield per plant and grain yield per plot.

High heritability coupled with high genetic advance as percent of mean was observed for no. of basal tillers per plant, no. of productive tillers per plant, main ear length, main ear width, finger length, total no. of fingers on the main ear, grain yield per plant and grain yield per plot. Thus, these traits are predominantly under the control of additive gene action and hence these characters can be improved by selection. High heritability with moderate genetic advance was recorded for plant height, no of leaves on the main tiller and finger width. These traits appear to be under the control of both additive and non-additive gene actions.

The variability for four qualitative characters viz., nodal pigmentation, degree of lodging at maturity, senescence and grain colour present in national collection of finger millet accessions are discussed in frequency. In case of nodal pigmentation genotypes without nodal pigmentation is more 64.58% frequency and genotypes with pigment is less with 35.41% frequency. Genotypes with higher susceptibility to lodging is higher in number among 48 genotypes with 66.66% frequency, genotypes with intermediate lodging having less genotypes than susceptible one with 27.08% frequency, genotypes with green colour at maturity is less in no with 27.08% frequency and genotypes without senescence occurred with 72.91% frequency. Genotypes having grain colour light brown occur with 45.83% frequency, copper brown with 43.7% frequency and purple brown with 10.41% frequency.

Highest yield was observed for the genotype (SNVD-11-118) and was showing presence of nodal pigmentation and lowest yield for the genotypes (CMLS-01-336-SEL-12) showing absence of nodal pigmentation. It has been clear from the result that nodal pigmentation had positive association with grain yield. The same genotype (SNVD-11-118) having light brown grain colour having higher yield which showed positive association of grain colour with grain yield. It has been recorded that higher yielding genotypes with intermediate lodging in maximum cases and also absence of senescence showed higher yield

Character association studies revealed that the characters grain yield per plant showed significant positive association with no. of basal tillers per plant, productive tillers per plant, main ear width, finger length, finger width, total fingers on the main ear and grain yield per plot. This indicated that simultaneous selection of all these characters was important for yield improvement.

Path coefficient analysis revealed that number of productive tillers per plant exerted the highest positive direct effect on grain yield per plant, followed by main ear width, finger length, finger width and grain yield per plot along with significant positive correlation for all the above mentioned characters.

A critical analysis of correlation and direct and indirect effects indicated that emphasis should be directed towards selection of parents having higher number of productive tillers per plant, main ear width, finger length, finger width and grain yield per plot.

Divergence studies through D^2 statistic indicated the presence of substantial diversity by forming large number of clusters with wide range of inter-cluster

distances. The multivariate analysis revealed that forty eight genotypes were distributed into 8 clusters. Out of eight clusters, cluster I was the largest comprising of thirty three genotypes followed by clusters II with five genotypes, cluster IV with four genotypes, cluster VIII with two genotypes and clusters III, V, VI, VII with one genotype each. The clusters III, V, VI and VII were represented by single genotype indicating high degree of heterogeneity among the genotypes.

Intra cluster D^2 values ranged from zero (cluster III, V, VI, VII) to 62.09 (cluster VIII). Maximum intra cluster distance was observed in cluster VIII (62.09), followed by cluster I (13.69), cluster II (10.95) and cluster IV (7.23). The intra cluster distance varied from a maximum 62.09 for cluster VIII to minimum 7.23 for cluster IV having 4 genotypes though it was zero for solitary clusters (III, V, VI, and VII) (Table 4.9). This reveals that genotypes occupying the same cluster have low level of diversity and selection of parents within the cluster may not be considered promising. From the inter cluster D^2 values of the eight clusters, it can be seen that the highest divergence occurred between cluster VI and VIII (1252.45), followed by cluster V and VIII (1235.52), cluster I and VIII (1224.30), cluster VII and VIII (1215.91), cluster III and VIII (1189.56), cluster IV and VIII (1160.76) and cluster II and VIII (1134.34).

The inter-cluster D^2 values were ranged widely with minimum value of 20.97 between clusters I and V and maximum value of 1252.45 between clusters VI and VIII indicating high diversity among the genotypes of these clusters. The maximum amount of heterosis is expected from the crosses with parents belonging to the most divergent clusters.

The data indicated that the cluster mean for plant height, no. of basal tillers per plant, productive tiller per plant and grain yield per plant was highest in cluster VII, no. of leaves on the main tiller was highest in cluster VI, ear width and finger length was recorded highest in cluster VIII. Cluster V recorded the highest finger width and highest grain yield per plot, Cluster IV recorded the highest main ear length. Cluster II recorded highest no. of total fingers per plant.

Higher yielder clusters are VII, I and II. Genotypes included in cluster VII is having highest mean value for grain yield per plant, total no. of basal tillers per plant and total productive tillers per plant. Cluster II is having highest mean value for no. of leaves on the main tiller and total fingers on the main ear. The genotypes SRYA-

333-SEL-2 (VII) as this cluster had only one genotype which become automatic choice, BAR-174 and SNVD-11-118 (I), SRS-13447 and SRS-13433 (II) from these clusters having high mean values for grain yield per plant may be directly used for adaptation or may be used as parents in future hybridization programme.

Among the 11 quantitative characters studied the most important character contributing to the divergence was main ear length followed by total no. of fingers on the main ear, grain yield per plot, grain yield per plant, main ear width, total no of basal tillers per plant, no. of leaves on the main tiller, total no. of productive tillers per plant, finger width, finger length. In order to select genetically diverse genotypes the material could be screened for the important traits viz., main ear length, total no. of fingers on the main ear, grain yield per plot, grain yield per plant, main ear width, total no. of basal tillers per plant.

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